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ARI17805 Sequence
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Unclassified.
1 (bases 1 to 10825)
Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D., Tsuchihashi,Z. and Wolff,R.K.
Hereditary hemochromatosis gene products
Patent: US 6140305-A 1 31-OCT-2000;
Location/Qualifiers
1. 10825
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AC090170 F
AC012430 F
AP002354 F
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ARI17789
ARI17789.1 GI:14098695
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AUTHORS
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JOURNAL
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AR117789
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                                                                                        June 19, 2002, 14:32:43; Search time 12601.5 Seconds (without alignments) 17976.355 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Qy	1081	GCCTGGAAAATTAAGTATATGTTAGTTTTGAACGTTTGAACTGAACAATTCTCTTTTCGG 114(40
qq	1081	CCTGGAAAATTAAGTATATGTTAGTTTTGAACGTTTGAACTGAACAATTCTCTTTTCGG 114	4
QY	1141	AGGCTTTATTGATTTGCAATGTGCTGTGTAATTAAGAGGCCTCTCTACAAAGTACTGA 120	
qu	1141	GTGTAATTAAGAGGCCTCTCTACAAAGTACTGA 120	
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QY	1561	AAATTTATTCAATGGTACACTGGGCTTTGGTGGCAGAGCTCATGTCTCCACTTCATAGC 16	Ñ
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QΥ	1621	9	280
qa	1621	ATGATICTIAAACATCACACIGCATTAGAGGITGAATAATAAAATTTCATGTTGAGCAG 16	580
QY	1681	ATTCATTGTTTACAAGTGTAAATGAGTCCCAGCCATGTGTGCACTGTTCAAGCCC 17	4
qq	1681	racaagreraaargagreecaagecargreragecacrerreaagece 17	740
Qy	1741	SAGAGCAGGGAAACAAGTCTTTACCCTTTGATATTTTGCATTCTAGTGGGAGA 18	0
qa	1741	GAGAGAGCAGGGAAACAAGTCTTTACCCTTTGATATTTTGCATTCTAGTGGGAGA 18	900
QY	1801	œ	٠
qa	1801	ATGACAATAAGCAAATGAGCAGAAAGATATACAACATCAGGAAATCATGGGTGTTGTGA 18	860
QY	1861	aagcagagaagtcagggaagtcactctgggggtgacacttgagcagagacatgaagga 19	Ċ.
qa	1861	CAGAGAAGTCAGGGCAAGTCACTCTGGGGCTGACACTTGAGCAGAGACATGAAGGA 19	Ò
Qy	1921	6	æ
qq	1921	SAATGATATTGACTGGGAGCAGTATTTCCCAGGCAAACTGAGTGGGCCTGGCAAG 19	æ
QY	1981	TIGGATIAAAAAGCGGGTITICICAGCACIACICAIGIGIGIGIGIGIGGGGGGGGGG	04
q O	1981	TIGGATTARARAGCGGGTTTTCTCAGCACTACTCATGTGTGTGTGTGTGGGGGGGG	04
QY	2041	CGCCTGGGGGTGGGAGGGGACTACCATCTGCATGTAGGATGTCTAGCAGTATCCTGT 21	9
ΩD	2041	CGGCGTGGGGGTGGGAAGGGGGGACTACCATCTGCATGTAGGATGTCTAGCAGTATCCTGT 21	10
QY	2101	÷.	16
qa	2101	CCTCCCTACTCACTAGGTGCTAGGAGCACTCCCCCAGTCTTGACAACAAAAATGTCTCT 21	

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5401 AGGAGAACAAC 5461 ACACAAATGG 5461 ACACAAATGA 5521 AACCTATAGAB 5521 AACCTATAGAB 111111111111111 5581 CTCATCCTTCC 5581 CTCATCCTTCC	5641 TCTTCAGTGAC 5641 TCTTCAGTGAC 5641 TCTTCAGTGAC 5701 AAGTGGCTGAA 5701 AAGTGGCTGAA 5761 CCCAATGGGGA 5761 CCCAATGGGGA 5761 CCCAATGGGGA 5821 CAGAGATATAC	5821 CAGAGATATAC 5881 GCTATGTGAC 5881 GGTATGTGACT 5941 TGAGGAGGTA 5941 TGAGGAGGTA 6001 GTGGCAATCA 6001 GTGGCAATCA 6001 GTGGCAATCA	6061 TAGTCATTGGF 	6241 AAGCATTTTTT 6241 AAGCATTTTTC 6301 AATGGTTCTCC 6361 TTTGCAAGAGC 6361 TTTGCAAGAGC 6421 TCTCAGAAGAGGC 6421 TCTCAGAAGAGGC 6421 TCTCAGAAGAGGCC 6481 ACCCCATGAGGCCCATGAGGCCCC
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	4561 AGGTTGCAGGCACGGAATCCCTGGTTGGAGTTTCAGAGGTGGCTGAGGCTGTGTGCCCTC	4741 GTGTCTATGGCTTGCTTTTATTTAACCAATAATCTTTTGTATATTTATACCGTTAA 4 11111111111111111111111111111111111	4921 4981 4981 5041 5101 5101	5161 ATATCAAGTGAGGCCACTTATCAGAGTAGAAGATCCTTTAGGTTAAAAGTTTCTTCAT 5220 5161 ATATCAAGTGAGGCCACTTATCAGAGAAGATCCTTTAGGTTAAAAGTTTCTTTC
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GCTGATCTGACTGCTCTCCAAGTGACACTGTGTTAGAGTCCAATCTTAGG 5460 CCAAATCTGGTAGGGAATGAAATGATAGCAAGTAAATGTAGTTAAAGAAG AGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCTAAAGACGTATTG ATTATGGCAGTGAGATGAGGATCTGCTCTTTGTTAGGGGGTGGGCTGAGG AGTCATCAGTGGAATTGCTGTTTTGTCGTCATCTTGTTCATGGAATTT GTCCTAAAGCAGGAAGCAAATGCTTAGGGTGTCAAAGGAAAGAATG CGINCCAGGIGGAGCACCCAGGCCTGGATCAGCCCCTCATIGIGAICTGG AAGGCTTTAACTTGCTTTTTCTGTTTTAGAGCCCTCACCGTCTGGCACCC ATTAAGGAAGAGGCAGGGTTCAAGTGAGTAGGAACAAGGGGGAAGTCTCT CTCATTTATATTCTTTGGGGACACCCAGCAGCTCCCTGGGAGACAGAAAT CCCCAGAATGAAAGTCTCTAATTCAACAACATCTTCAGAGCACCTACTAT CTGTTTAAGGTAGTACAGGGGCTTTGAGGTTGAGAAGTCACTGTGGCTAT AGGAAGTGAAAGTTCCAGTCTTCCTGGCAAGGGTAAACAGATCCCCTCTC CTCTTTCCTGTCAAGTGCCTCCTTTGGTGAAGGTGACACATCATGTGACC CCACTCTACGGTGTCGGGCCTTGAACTACTACCCCCCAGAACATCACCATG ATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAG TGATGAGAGCCAGGAGCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCC

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	ATCACATTCAGCTGGGGATCAAGATAGCCTTCTGGATCTTGAAGGAGAAGATGCTGGTTCCA 6	TTAGGTGAGGTTGAAGATGATGAGAGGTCTACACAGACGGAGCAACCATGCCAAGTAGGA 66	GAGTATAAGGCATACTGGGAGATTAGAAATAATTACTGTACCTTAACCCTGAGTTTGCGT 67	AGCTATCACTCACCAATTATGCATTTCTACCCCCTGAACATCTGTGGTGTAGGGAAAAGA 67	GAATCAGAAAGAAGCCAGCTCATACAGAGTCCAAGGGTCTTTTGGGATATTGGGTTATGA 68 	TCACTGGGGTGTCATTGAAGGATCCTAAGAAAGGAGACCACGATCATCATATATGGTG 69	AATGTGTTGTTAAGAAGTTAGATGAGGGGGGGACCAGTTAGAAAGCCAATAAGCAT 69	TTCCAGATGAGAGATAATGGTTCTTGAAATCCAATAGTGCCCAGGTCTAAATTGAGATGG 702 	GTGAATGAGGAAAATAAGGAAGAGAGAAGAGGCAAGATGGTGCCTAGGTTTGTGATGCCT 708 	CTTTCCTGGGTCTCTTGTCTCCACAGGAGCCCATGGGGCACTACGTCTTAGGTGACG 714	TGAGTGACACGCGGCTGCAGACTCACTGTGGGAAGGAGACAAAACTAGAGACTCAAAGA 7 	GGGAGTGCATTTATGAGCTCTTCATGTTCAGGAGAGAGAG	GCCTGACGAACTCCTTGATTTTAGCCTTCTGTTCATTTCCTCAAAAGATTTCCCCAT	TTAGGTTTCTGAGTTCCTGCATGCCGGTGATCCCTAGCTGTGACCTCTCCCCTGGAACTG 7 [TCTCTOATGAACCTCAAGCTGCATCTAGAGGCTTCCTTCATTTCCTCCGTCACCTCAGAG 744	ACATACACCTANGTCANTTCANTTCCTATTTTGGAAGAGGACTCCTTAAATTTGGGGA 7	CTTACATGATTCATTTTAACATCTGAGAAAGCTTTGAACCTGGGACGTGGCTAGTCAT CTTACATGATCATTTTAACATCTGAGAAAGCTTTGAACCCTGGGACGTGGCTAGTCAT CTTACATGATCATTTTAACATCTGAGAAAGCTTTGAACCTGGGACGTGGTAGTAA	AACCTTACCAGATTTTTACACATGTAFCTATGCATTTTCTGGACCGGTTCAACTTTTCCT 7

8160 8160 8220 8220 ATAAAAATACAAAAATTAGCTGGGGGTGGTGGGGG 8280 7800 7860 7920 ACAATAATTCTATGAGATAGGTACTATTATCCCCAT 8100 AGTAACTCATCTGTCACCAAGCCTTGGGGATTCTTC 7680 CAGCTATGAAGGCTGTACACTGCACGAATGGAAGAG 7740 CITACITCGIGICCGACICITCIGAGCACCIACITA 8040 AAGGCTGAGGCAGGAGAATGGCATGAACCCAGGAGG 8340 GCGCCACTGCACTCCAGCCTAGGTGACAGAGTGAGA 8400 ACTCCCTTGCTCCTCTGTTGCTCTTTGGCATTCA 8760 AGTAGGCCGGCACGGTGGCTCACGCCTGTAATCCC AGTAGGCCGGCCACGTGCCTCACGCCTGTAATCCC GATAGAAACAGGTTTCAAACTCAGTCAATCTGACCG CTCATTGTGTTTCTTCAGTGAGCTTGAATCACAT CTCATTGTGTTTCTTCTGAGTGAGCTTGAATCACAT AACTGATCCTCAGCTGTCATGTTTCCTTTAAAAGTC TGGATCACGAGGTCAGGAGATCGAGACCATCCTGGC GGGGTTGTGAAGAGGTGTTTTTTTTAATTGGCATGA TGGCTATCTGTGGGTAGTATGATGGGTGTTTTTAGC TTAATGGTGCCTTCATTTGGGATGCTACTCTAGTAT

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Oy Db	2941	TTCTGAGATGGTGAAGGCAGGGAAAGAGCAGTTTGGGGTAAATCAAGGATCTGCATTTG 3000
QY		TTTGAGATTCCAGTCAGGCTTCCAAGTGGTGAGGCCACATAGGCAGTT
Qy	3061	GAATTCAGGACCAAGGCTGGCCACGGTGGCTCACTTCTGTAATCCCAGCAC
QY	3121	TTGAGGTCAGGAGTTTGAGACAAGCTTGGCCAACA 31
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QY	3361	AGGAATTATTCCTCAGGATTTGGG 34
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Qy Dp	3481	AATCATGAGTATTGGAATAGGAT 35
Qy	3541	GGCAGTGAGGGGTGGCACCTGTGTGGCAGAAAAGCACACAAGAAAGGC 36;
QY	3601	GACTGTCATATGGAAGAAGACAGGACTGCAACTCACCCTTCACAAATGAGGA 366
QY	3661	CCAGACACACAGTGATGATGAGTTGATGCAGGTGTGTGGAGCCTCAACATCCTGCTCC 372
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Qy		CCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTTCTTTCCTTGTTTGAAGCTTTGGGCTA 384
Qy	3841	CGTGGATGACCAGCTGTTCGTGTTCTATGATNATGAGAGTCGCCGTGTGGAGCCCCCGAAC 390
QY	3901	TCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGCAGCTGAGTCAGAGTCTGAA 3
Qy	3961	AGGTGGGATCACATGTTCACTGTTCTGGACTATTATGGAAAATCACAACCACAG 4

000	408	4140	4200	4260	4320	4380 4380	4440	4500	4560 · 4560	4620 4620	4680	4740	4800	4860	4920	4980	5040	5100	6160
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5400 5460 5940 6180 6240 5400 5460 5520 5520 5580 5580 5640 5640 5700 5700 5760 5760 5820 5820 5880 5880 5940 0009 0009 0909 0909 6120 6120 6180 TAGTACCTCTGCCCCAGGGCACAGTGGGAAGAGGGGCAGAGGGGGATCTGGCATGGG **AGGGCAATITITATCTATCAGAACAAGAACATGGGTAACAGATATGTATATTACATGTG** AACCTATAGAAGGAAGTGAAAGTTCCAGTCTTCCTGGCAAGGGTAAACAGATCCCCTCTC TCTTCAGTGACCACTCTACGGTGTCGGGCCTTGAACTACTACCCCCAGAACATCACCATG CCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAG GGTATGTGACTGATGAGAGCCAGGAGCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCC TCAGGAGGTAATTATGGCAGTGAGATGAGGATCTGCTCTTTGTTAGGGGGTGGGCTGAGG GTGGCAATCAAAGGCTTTAACTTGCTTTTTTTTTAGAGCCCTCACCGTCTGGCACCC TAGICATIGGAGICAICAGIGGAATIGCIGITTITIGICGICATCTIGITCAIIGGAATIT AGAACATAGCAATAATCACTGAAGCTACCTATCTTACAAGTCCGCTTCTTATAACAATGC CTCCTAGGTTGACCCAGGTGAACTGACCATCTGTATTCAATCATTTTCAATGCACATAA AGGAGAACAAGCTGATCTGACTGCTCTCCAAGTGACACTGTGATAGAGTCCAATCTTAGG 5401 AGGAGAACAGGTGATCTGACTGCTCTCCAAGTGACACTGTTAGAGTCCAATCTTAGG CTCATCCTTCCTCTTTCCTGTCAAGTGCCTCCTTTGGTGAAGGTGACACATCATGTGACC AAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCTAAAGACGTATTG TGTTCATAATATTAAGGAAGGCAGGGTTCAAGTGAGTAGGAACAAGGGGGAAGTCTCT 5941 6061 6121 5461 5641 6061 6181 5281 5641 5701 5761 6001 6001 6121 5101 5221 5221 5281 5341 5401 5461 5521 5521 5581 5701 5761 5821 5821 5881 5881 5941 qq qq qq g ΩŽ a Ω δy ò δ g Οý Q δλ g δy g ŏ g οy qq οy qq QΥ ΩD δy 셤 δ g οy δ g Qγ qq Ω

g	6181	TAGTACCTCTGCCCCAGGGCACAGTGGGAAGAGGGGCAGAGGGGGATCTGGCATCCATGGG 6240
ò	6241	CATTTTTCTCATTTATATTCTTTGGGGACACCAGCAGCTCCCTGGGAGACAGAAAT 630
. g	6241	
ç,	6301	AATGGTTCTCCCCAGAATGAAAGTCTCTAATTCAACAAACA
oy Ob	6361 6361	TTTGCAAGAGCTGTTTAAGGTACTACAGGGCTTTGAGGTTGAGAAGTCACTGTGGCTAT 6420
QY Ob	6421 6421	TCTCAGAACCCAAATCTGGTAGGGAATGAAATTGATAGCAAGTAAATGTAGTTAAAGAAG 6480
y d	6481 6481	ACCCCATGAGGTCCTAAAGCAGGCAGGAAGCAATGCTTAGGGTGTCAAAGGAAAGAATG 6540
Oy Op	6541 6541	ATCACATICAGCIGGGGATCAAGATAGCCTICTGGATCTTGAAGGAGAAGCTGGATTCCA 6600
dy Db	6601	TTAGGTGAGGTTGAAGATGATGGGAGGTCTACACAGAGGAGCAACCATGCCAAGTAGGA 6660
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Qy Dp	7021	GTGAATGAGGAAAATAAGGAAGAGAGAAGAGGCAAGGTGGTGCCTAGGTTTGTGATGCCT 7080
Oy Dp	7081	CTTTCCTGGGTCTCTTGTCTCCACAGGAGCATGGGGCACTACGTCTTAGCTGAACG 7140
Oy Dp	7141	TGAGTGACACGCAGCCTGCAGACTCACTGTGGGAGAGACAAAACTAGAGACTCAAAGA 7200
oy Op	7201	GGGAGTGCATTTATGAGCTCTTCATGTTTCAGGAGAGTTGAACCTAAACATAGAAATT 7260
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Oy	7321	m	0
qq		TAGGTTTCTGAGTTCCTGCATGCCGGTGATCCCTAGCTGTGACCTCTCCCCTGGAACTG 73	0
QY	m	TCTCTCATGAACCTCAAGCTGCATCTAGAGGCTTCCTTCATTTCCTCCGTCACCTCAGAG 7440	0
qa	7381	CTCTCATGAACCTCAAGCTGCATCTAGAGGCTTCCTTCATTTCCTCCGTCACCTCAGAG 74	0
δλ	7441	ACACCIATGICATITCATTICCIAITTITGGAAGAGGACTCCTIAAAITIGGGGGA 75	0
qa	7441	ATACACCTATGTCATTTCCTATTTTTGGAAGAGACTCCTTAAATTTGGGGGA 75	0
٥٨	i û	CATGATTCATTTAACATCTGAGAAAAGCTTTGAACCTGGGAC	0 (
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Qy	56.	AACCTTACCAGATTTTTACACATGTATCTATGCATTTTCTGGACCCGTTCAACTTTTCCT 7620	0
qq		CTTACCAGATTTTTACACATGTATCTATGCATTTTCTGGACCCGTTCAACTTTTCCT 76	0
Qy	7621	CCUGICITACCCAGIAACICAICIGICACCAAGCCITGGGGAIICIIC 76	0
qq	7621	TGAATCCTCTCTGTGTTACCCCAGTAACTCATCTGTCAAACCTTGGGGATTCTTC 76	0
Qy	7681	TGATTGTGATGTGAGTTGCACAGCTATGAAGCCTGTACACTGCACGAATGGAAGAG 77	0
Оb	1681	ATCTGATTGTGATGTGAGTTGCACAGCTATGAAGGCTGTACACAGGCAGG	0
QY	7741	GTCCCAGAAAAACCATCATGGCTATCTGTGGGTAGGATGGGTGGG	0
qq	7741	CACCTGTCCCAGAAAAAGCATCATGGCTATCTGTGGGTAGTATGATGATGTGTTTTTAGC 7E	0
Qy	7801	GAGGCAAATATCTTGAAAGGGGTTGTGAAGAGGTGTTTTTTCTAATTGGCATGA 76	0
qq	7801	GGTAGGAGCCAAATATCTTGAAAGGGGTTGTGAAGAGGTGTTTTTTTT	0
Qy	7861	TGCAAAGTTTAATGGTGCCTTCATTTGGGATGCTACTCTAGTAT 75	0
qa	7861	GGTGTCATACAGATTGCAAAGTTTAATGGTGCCTTCATTTGGGATGCTACTCTAGTAT 75	0
Qy	7921	CAGACCIGAAGAAICACAATAATITICIACIGGICICICCTIGITCIGAIAAIGAAA 75	0
qq	7921	CCAGACCTGAAGAATCACAATAATTTTCTACCTGGTCTCTTCTTGTTCTGATAATGAAA 79	0
Qy	7981	GATAAAAGCACTTACTTCGTGTCCGACTCTTCTGAGCACCTACTTA 80	0
QQ	7981	rargaraaggargaraaaagcacrracrrcgrgrccgacrcrrcrgagcaccracrra 80	0
Oy	4	CTGCATGCACTTCTTACAATAATTCTATGAGATAGGTACTATTATCCCCAT 81	0
Dp	8041	GCATTACTGCATGCACTTCTTACAATAATTCTATGAGATAGGTACTATTATCCCCAT 81	0
Οy	8101	TICITITITAAAIGAAGAAAGIGAAGIAAGCCGGCACGGGCTCACGCCTGTAATCCC 8160	0
QQ	8101	TOTITITITAAATGAAGAAAGTGAAGTAGGCCGGGCACGGTGGCTCACCCCTGTAATCCC 81	0
Qy	8161	TTGGGAGGCCAAAGCGGGTGGATCACGAGGTCAGGAGATCGAGACCATCCTGGC 82	0
qq	8161	JACTITIGGGAGGCCAAAGCGGGTGGATCACGAGGTCAGGAGATCGAGACCATCCTGGC 82	0
Oy	8221	ACATGGTGAAACCCCATCTCTAATAAAAATACAAAAAATTAGCTGGGCGTGGTGGCGG 82	
QQ	8221	AAAAATACAAAAATTAGCTGGGCGTGGTGGCAG 828	
ΟÝ	8281	CCTGTAGTCCCAGCTACTCGGAAGGCTGAGGCAGGAGAATGGCATGAACCCAGGAGG 83	0
QQ	8281	CCCTGTAGTCCCAGCTACTCGGAAGGCTGAGGCAGGAATGGCATGAACCCAGGAGG 834	0
Qy	8341	TIGCAGIGAGCCGAGITIGCGCCACTGCACTCCAGCCTAGGIGACAGAGTGAGA 84	0
Db	8341	3AGCTTGCAGTGAGCCGAGTTTGCGCCACTGCACTCCAGCCTAGGTGACAGAGTGAGA 8	0

Qy 84	401 CTCCATCTCAAAAAAATAAAATAAAATAAAAATGAAAAAAAA	460
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Qy 84 Db 84	461 TAGAGTATCTCAPAGTTTGTCAGTGATAGAAACAGGTTTCAAACTCAGTCAATCTGACCG 8: 	520 520
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Qy 85	581 GGAAGGAGATGGCTCTTCTCTCTCTCTCTTCTGAGTGAGCTTGAATCACAT 8	64
0 00 0	641 GAAGGGGAACAGCAGAAAACAACCAACTGATCCTCCAGCTGCAGTGTGCTTTAAAACT 8	70
co	641 GAAGGGGAACAGCAGAAAAACAACCAACTGATCCTCAGCTGTCTTGTTTAAAAGTC 8	70
OY 87 Db 87	701 CCIGAAGGAAGGTCCTGGAATGTGACTCCCTTGCTCCTGTTGCTCTTTGGCATTCA 8	760 760
Oy 87 Db 87	761 TTTCTTTGGACCCTACGCAAGGACTGTAATTGGTGGGGACAGCTAGTGGCCCTGCTGGGC 8:	820 820
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Qy 88 Db 88	881 CCTCAATGAAGTGGAGTAAGCTCTCTCATTTTGAGATGGTATAATGGAAGCCACCAAGTG 8 	940 940
Qy 89 Db 89	941 GCTTAGAGGAIGCCCAGGICCTTCCATGGAGCCACTGGGGTTCCGGTGCACATTAAAAA 9	000
QY 90 DP 90	001 AAAATCTAACCAGGACATTCAGGAATTGCTAGATTCTGGGAAATCAGTTCACCATGTTCA 9	090
06 qa	061 AAAGAGTCTTTTTTTTTTTTTTGAGACTCTATTGCCCAGGCTGGAGTGCAATGGCATGAT 9	120 120
Qy 91 Db 91	121 CTCGGCTCACTGTAACCTCTGCCTCCCAGGTTCAAGCGATTCTCCTGTCTCAGCCTCCCA 9	180 180
Qy 91 Db 91	181 AGTAGCTGGGATTACAGGCGTGCACCACGATGCCCGGCTAATTTTTGTATTTTTAGTAGA 9: 11111111111111111111111111111111111	240 240
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Oy 93	361 AGAGTCTTAATATATATATCCAGATGCCATGTGTTTACTTTATGTTACTACACACTTG 9.	420
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	9601	ACGCTCATTGTAGAAAAGCTATAAAATGAATACAATTAAAACTGTTATTTAATTAGCCAG 966	
	9661	TGAAAAACTATTAACAACTIGICIAITAACCIGITAGTATTATIGITGCTIAAAAAIGCA 973	
	9721 9721	TATACTTTAATAAANGTATATTGTATAGTATACTGCATGATTTTATTGTAAGTTCTTGTTC 978	
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oy Ob	9841	CTTTACATTTTGTCTTACGGAATATTTTCATTCAACTGTGGTAGCCGAATTAATCGTGT 99(
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O.Y DD	9961	CATTCTGAAAGCATATGACAAATTATTCTCTCTTAATATCTTACTACTATACTGAAAGCAGA 100	
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QY Db	10321	CATTITAAAITCTTATTCACCTCTGGCAAAACCATTCACAAACCATGGTAGTAAAGAGAA 10:	0380
Oy Dp	10381 10381	GGGTGACACCTGGTGGCCATAGGTAAATGTACCACGGTGGTCCGGTGACCAGAGATGCAG 10.	
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QY	10501	ATCACTTGTAGAGAAAAGCCCTGAAAATTTGAGAAAACAAAAGAAAG	.0560
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                     AAGGAAAACAAACCACTCTGATAATCATTGAGTCAAGTACAGCAGGTGATTGAGGACTGC
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Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D. Tsuchinsshi,Z. and Wolff,R.K.
Tsuchinsshi,Z. and Wolff,R.K.
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Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D., Tsuchihashi,Z. and Wolff,R.K.
Hereditary hemochromatosis gene products
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QY	3481	ATTICTAGAATCCACCAGCTTTAGTGGAGTCTGTCTAATCATGAGTATTGGAATAGGAT 3540 	
QY	3541	CTGGGGCAGTGAGGGGTGGCAGCGTGGCAGAGAAAGCACACAAGGAAAGGC 3600 	
QY	3601	ACCCAGGACTGTCATATGGAAGAAAGACAGGACTGCAACCCTTCACAAAATGAGGA 3660 	
QY Dp	3661	CCAGACACAGCTGATGGTATGAGTTGATGCAGCTGTGGGAGCCTCAACATCCTGCTCCC 3720 	
Qy	7 7	ACTACACATGGTTAAGGCCTGTTGGTCTGTCTCGAGGTTCACACTCTCTGCACTA 378	
Qy Db	3781	CCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTGTTTGAAGCTTTGGGCTA.3840 	
Qy	3841	CGTGGATGACCAGCTGTTCGTGTTCTATGATNATGAGAGTCGCCGTGTGGAGCCCCGAAC 3900 	
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QY	4381	TGGCCCACCAAGCTGGAGTGGGAAAGGCACAAGATTCGGGCCAGGCAGAACAGGGCCTAC 4440 	
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81 81	ATTATGATAAGGATGATAAAAGCACTTACTTCGTGTCCGACTCTTCTGAGCACCTACTTA	8040 8040
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61	AGCACTITIGGGAGGCCAAAGCGGGTGGATCACGAGGTCAGGAGATCGAGACCATCCTGGC	8220 8220
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41	CAGAGCTTGCAGTGAGCCGAGTTTGCGCCACTGCACTCCAGCCTAGGTGACAGTGAGA	8400 8400
01	CTCCATCTCAAAAAAATAAAAATAAAAATAAAAAATGAAAAAAAA	8460 8460
461	TAGAGTATCTCATAGTTTGTCAGTGATAGAAACAGGTTTCAAACTCAGTCAATCTGACCG 	8520 8520
521 521	TITGATACATCICAGACACCACTACATICAGTAGTTTAGATGCCTAGAATAAATAGAGAA 	8580 8580
581 581	GGAAGGAGATGGCTCTTCTCTTGTCTCATTGTGTTTCTTCTGAGTGAG	8640 8640
641 641	GAAGGGGAACAGCAGAAAACCAACTGATCCTCAGCTGTCATGTTTCCTTTAAAAGTC	8700 8700
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61 61	TITCTITGGACCCTACGCAAGGACTGTAAITGGTGGGGACAGCTAGTGGCCCTGCTGGGGCCTTGTTTTTTTT	8820 8820
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Tsuchihashi,2. and Wolff,R.K.
Method for determining the presence
hemochromatosis gene mutation
Patent: US 6228594-A 1 08-MAY-2001;
                          Location/Qualifiers
                                        /organism="unknown"
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         CCAGTCTTCACAGTAACACATTTCACTAACACATTTACTAAACATCAGCAACTGTGGCCT
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  CATTCTGAAAGCATATGACAAATTATTTCTCTTTAATATCTTACTATACTGAAAGCAGA
                            AGGTAAGCATTTGTTTTATATTTGGTTTTTTTTCACCTGGGCTGAGATTTCAAGAAACACC
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81	GCCACAAACAAGGTTGTGCAGGCGCCTGTAGGCTGTGTGTG	2340
41	- ACAGTGATCTGTCACAGGCTTTTAAAAGATTGCTCTGGCTGG	2400
01	- AAGGGAGCAACAGTAAAAGCAGGGAGCCCAGGAAGGAGCTGTTACACAGTCCAGGCAAG	2460
61 61	- AGGTAGTGGAGTGGGCTGGGTAACAGAAAAGGGAGTGACAAACCATTGTCTCCTGAA 	2520
21	TATATTCTGAAGGAAGTTGCTGAAGGATTCTATGTTGTGTGAGAGAAAGAGAAATTGG 	2580
81	CTGGGTGTAGTAGCTCATGCCAAGGAGGCCAAGGAGAGCAGATTCCTGAGCTCAGGA 	2640
41	GITCAAGACCAGCCIGGGCAACACCAGCAAAACCCCITCTCTACAAAAAAAAAA	2700
01	GCTGGGTGTGGTGCATCCTGTGATCCTACTACTCGGAGGCTCAGGTGGAGGTTGTT	2760
61 61	TIGCITGAGCCCAGGAAGITGAGGCTGCAGTGACCATGACTGTGCCACTGTACTTCAGC	2820
21	CTAGGTGACAGAGCCAAGACCCTGTCTCCCCTGACCCCCTGAAAAAGAGAAGAGTTAAAGT 	2880
81	GACTITGITCITIAITITAAITITAAITGGCCTGAGCAGTGGGGTAAITGGCAATGCA 	2940
41	JTGAGATGGTGAAGGCAGAGGAAAGAGCAGTTTGGGGTAAATCAAGGATCTGCATT 	3000
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89	841	AAAGGATCCTAAGAAAGGAGCACCACGATCTCCCTTATATGGT 690
69	901	TAAGAAGTTAGATGAGAGGTGAGGAGACCAGTTAGAAAGCCAATAAGCAT
69	961	GAGAGATAATGGTTCTTGAAATCCAATAGTGCCCAGGTCTAAATTGAGATGG 702
70	021	GGAAAATAAGGAAGAGAGAGAGGCAAGATGGTGCCTAGGTTTGTGATGCCT 7
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71	141 141	CAGGCAGCCTGCAGACTCACTGTGGGAAGGAGACAAAACTAGAGACTCAAAGA 72
72	201	TPATGACCTCTTCATGTTTCAGGAGAGAGTTGAACCTAAACATAGAATT 726
72	261	CGAACTCCTTGATTTTAGCCTTCTCTGTTCATTTCCTCAAAAGATTTCCCCAT 7
73	321	TGACTTCCTGCATGCCGGTGATCCCTAGCTGTGACCTCTCCCCTGGAACTG 738
73	381	TTCCTTCATTTCCTCCGTCACTCAGAG 7.

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b 24	7681 7681	CATCTGATTGTGATGTGAGTTGCACAGCTATGAAGGCTGTACACTGCACGAATGGAAGAG 7740 	
λ Q Q	7741	GCACCTGTCCCAGAAAAAGCATCATGGCTATCTGTGGGTAGTATGATGGGTGTTTTTAGC 7800 	
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864	1. GAAGGGGAACAGCAGAAACCAACTGATCCTCAGCTGTCATGTTTCCTTTAAAAGTC 8700
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876	1 TITCITIGGACCCTACGCAAGGACIGIAATIGGIGGGGACAGCIAGTGGCCCCTGCTGGGC 8820
8	1 TTCACACACGGTGTCCTCCCTAGGCCAGTGCCTCTGGAGTCAGAACTCTGGTGGTATTTC 888
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00	1 AAAAICTAACCAGGACATICAGGAATIGCIAGATICIGGGAAATCAGTICACCAIGTICA 906
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912	11 CTCGGCTCACTGTAACCTCTGCCTCCCAGGTTCAAGCGATTCTCCTGTCTCAGCCTCCCA 9180
	1 AGTAGCTGGGATTACAGGCGTGCACCACGATGCCCGGCTAATTTTTTAGTAGA 92
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930	1 IGCCICGGCCICCCAAAGIGCIGAGATTACAGGIGIGAGCCACCCTGCCCAGCCGICAAA 936
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936	51 AGACTCTTAATATATATCCAGATGCCATGTTTACTTTATGTTACTTAC
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948	1 ACAGCTCAGAAGTTTCTTCT
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954	11 TTAAACCATTTTCTTTTTTTGTGGTTAGAAAAGTTATGTAGAAAAAGTAAAATGTGATTT 9600
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096	01 ACGCTCATTGTAGAAAAGCTATAAAATGAATACAATTAAAGCTGTTATTTAATTAGCCAG 9660

GCTGTTATTTAGCCAG 9660	IGTTGCATTAAAAATGCA 972	TATTGAAGTTCTTGTT		TTTATTTTGCTTCTAATTT 9840 	AATTAATCGTGTT 990	090	GGITATITACCAGCAAAC 9900 GGTTATITATCCAGCAAAC 9960	TTCTCTCTTAATATCTTACTATACTGAAAGCAGA 10020 	ATGTTACAATTAATTTATT 10080 	TGAGATTTCAAGAACACC	AACTGTGGCCT 1020	ACCAACIGIGGCCI 102 TITITIAAGCTTAA 102	TGAAAAATCAAAGACCTG 1032	CCATGTAGTAAAGAGA 1038	SACCAGAGATGCAG 1044 	GGAGGGGCTGCACTGGAA 10500 	ACTTACCAG 1056	ACACAACAG 1062 ACACAACAG 1062	TGATTGAGGACTGC 1068 TGATTGAGGACTGC 1068	TCTTATAATACTGT 1074
ACGCTCATTGTAGAAAGCTATAAAATGAATACAATTAAAG	AAACTATTAACAACTIGICIATTACCIGITAGIATT	ATACTTTAATAAATGTATATTGTATTGTATACTGCA		ATCTIGTGTATATACTTAATCGCTTTGTCATTTTGGAGACATTTTTT 	CTTTACATTTGTCTTACGGAATATTTCATTCAACTGTGG 	IACAITITGICITACG ICACICIAGGGACAIT		CATTCTGAAAGCATATGACAAATTATTTCTCTCTTAATATC 	CTGCTATAAGGCTTCACTTACTCTTCTACCTCATAAGAATAN 	AGGTAAGCATTTGTTTTATATTGGTTTTATTTCACCTGGGCTGAGATTT 	3TAACACATTTCACTAACA	TITTTTTAATAGAAATTTAAGTCCTCAT	CTTTATTCATAAATTCTTAAGGTCAACTAC	ATTTTAAATTCTTATTCACCTCT	GGGTGACACCTGGTGGCCATAGGTAAATGTACCACGGTGGT 	CGCTGAGGGTTTTCCTGAAGGTAAAGAATAAAGAATGGGT(CAA	CTATTTGAATTGCTGGAATCACAGGCCATTGCTGAGCTGCC 	AAGTAC 	₽
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1 (bases 1 to 10825)
Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D.,
Tsuchihashi,Z. and Wolff,R.K.
Method for determining the presence or absence of a hereditary
hemochromatosis gene mutation
Patent: US 6228594-A 3 08-MAY-2001;
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Sequence 3 from patent US 6228594.
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qq	2701	GCTGGGTGTGGTGGCATGCACCTGTGATCCTAGCTACTCGGGAGGCTGAGGTGGAGGGTA 2760	
O.Y OD	2761 2761	TIGCTICAGCCCAGGAAGTIGAGGCTGCAGTGAGCCAIGACTGIGCCACTGTACTICAGC 2820 	
Qy Db	2821	CTAGGTGACAGAGCAAGACCCTGTCTCCCTGACCCCCTGAAAAGAGAGAG	
QQ Dp	2881	TGACTITGITCITIATITIAATITIATITGCCIGAGCAGIGGGGTAATIGGCAATGCCAT 2940 	
Qy Db	2941	TTCTGAGATGGTGAAGGAAGGAAGGAGTTTGGGGTAAATCAAGGATCTGCATTTG 3000 	
Qy Db	3001	GGACAIGTTAAGTTTGAGATTCCAGTCAGGCTTCCAAGTGGTGAGGCCACATAGGCAGTT 3060 	
Oy Dp	3061	CAGTGTAAGAATTCAGGACCAAGGCTGGGCACGGTGGCTCACTTCTGTAATCCCAGCACT 3120 	
OY Db	3121	TTGGTGGCTGAGGCAGGTAGATCATTTGAGGTCAGGAGTTTGAGACAAGCTTGGCCAACA 3180 	
Q _Y	3181	TGGTGAAACCCCATGTCTACTAAAAATACAAAAATTAGCCTGGTGTGGTGGCGCACGCCT 3240 	
Qy	3241	ATAGTCCCAGGTTTTCAGGAGGCTTAGGTAGGAATCCCTTGAACCCAGGAGGTGCAGG 3300 	
QY Dp	3301	TIGCAGIGAGCIGAGAITGIGCACTGCACTCCAGCCTGGGTGATAGAGTGAGACTCTGT 3360 	
QY	3361 3361	CTCAAAAAAAAAAAAAAAAAAAAAAAAAAACTGAAGGAATTATTCCTCAGGATTTGGG 3420 	
Qy	3421	TCTAATTTGCCCTGAGCACCAACTCCTGAGTTCAACTACCATGGCTAGACACACTTAAC 3480 	
QY Dp	3481	ATTICTAGAATCCACCAGCTITAGTGGAGTCTGTCATCATGAGTATTGGAATAGGAT 3540	
Qy Dp	3541	CTGGGGGCAGTGAGGGGGGGGGCGCGCGTGTGGCAGAAAAGCACACAAGGAAAGACC 3600 	
Qy Db	3601	ACCCAGGACTGTCATATGGAAGAAGACAGGACTGCAACTCACCCTTCACAAAATGAGGA 3660 	
Qy	3661	CCAGACACAGCTGATGGTATGAGTTGATGCAGGTGTGTGGAGCCTCAACATCCTGCTCCC 3720 	
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Method for determining the presence or hemochromatosis gene mutation
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4500 4440 4440 4500 4560 4620 4260 4260 4320 4320 4380 4380 4080 4140 4200 4200 3900 3540 3720 3780 3780 AGGTTGCAGGGCACGGAATCCCTGGTTGGAGTTCAGAGGTGGCTGAGGCTGTGTGCCTC GAATTTGCTTCCTGAGATCATTTGGTCCTTGGGGATGGTGGAAATAGGGACCTATTCCTT TGGCCCACCAAGCTGGAAAGGCACAAGATTCGGGCCAGGCAGAACAGGGCCTAC CTGGAGAGGGACTGCCCTGCACAGCTGCAGTTGCTGGAGCTGGGGAGAGGTGTTTTG GACCAACAAGGTATGGTGGAAACACACTTCTGCCCCTATACTCTAGTGGCAGAGTGGAGG CGTGGATGACCAGCTGTTCGTGTTCTATGATNATGAGAGTCGCCGTGTGGAGCCCCGAAC TGGTTGCAGTTAACAAGGCTGGGGATTTTTCCAGAGTCCCACACCCTGCAGGTCATCTG CTCCTACTACACATGGTTAAGGCCTGTTGCTCTGTCTCCAGGTTCACACTCTCTGCACTA CCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCTTGTTTGAAGCTTTGGGCTA AGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTATGGAAAATCACAACCACAG CTGGGGGCAGTGAGGGGGTGGCCACGTGTGGCAGAAAAAGCACACAAGGAAAGAGC 4381 4381 4441 4501 4201 4441 4501 4561 3961 4081 4081 4201 3901 3901 4021 4021 4141 3841 3961 3541 3601 3661 3721 3721 3781 3781 3841 3481 3541 3601 3661 g 9 ò q οy Db qq g δ g δ g Ω qq ōλ Óγ QQ g οy рp δλ g δy g QΥ qq οy d QYΩ qq QY δy QΥ

5820 0009 0009 0909 0909 6120 6180 6180 6240 6240 6300 6360 6360 6420 6480 6540 6540 0099 5820 5880 5940 5940 6120 TGAGGAGGTAATTATGGCAGTGAGATGAGGATCTGCTCTTTGTTAGGGGGTGGGCTGAGG TGAGGAGGTAATTATGGCAGTGAGATGAGGATCTGCTCTTTGTTAGGGGGTGGGCTGAGG 6421 TCTCAGAACCCAAATCTGGTAGGGAATGAAATTGATAGCAAGTAAATGTAGTTAAAAGAAG ACCCCATGAGGTCCTAAAGCAGGAGGAAGCAAATGCTTAGGGTGTCAAAGGAAAGAATG AGCTATCACTCACCAATTATGCATTTCTACCCCCTGAACATCTGTGTGTAGGGAAAAGA CCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCCCTGGGGAAGAG CAGAGATATACGINCCAGGIGGAGCACCCAGGCCIGGATCAGCCCCTCATIGIGATCTGG GGTATGTGACTGATGAGAGCCAGGAGCTGAGAAAATCTATTGGGGGGTTGAGAGGAGTGCC TAGTCATTGGAGTCATCAGTGGAATTGCTGTTTTTGTCGTCATCTTGTTCATTGGAATTT TGTTCATAATATAAGGAAGAGGCAGGGTTCAAGTGAGTAGGAACAAGGGGGAAGTCTCT TAGTACCTCTGCCCCAGGGCACAGTGGGAAGAGGGGCAGAGGGGGATCTGGCATCCATGGG AAGCATTTTTCTCATTTATATTCTTTGGGGACACCAGCAGCTCCCTGGGAGACAGAAAAT AATGGTTCTCCCCAGAATGAAAGTCTCTAATTCAACAACATCTTCAGAGCACCTAAT ATCACATTCAGCTGGGGATCAAGATAGCCTTCTGGATCTTGAAGGAGAAGCTGGATTCCA #TAGGTGAGGTTGAAGATGATGGGAGGTCTACACAGACGGAGCAACCATGCCAAGTAGGA GAGTATAAGGCATACTGGGAGATTAGAAATAATTACTGTACCTTAACCCTGAGTTTGCGT 6241 6301 6481 6481 6241 6301 6421 6541 6541 6601 6721 5701 5761 5821 5941 5941 6001 6061 6121 6121 6181 6601 1999 6661 6721 5701 5761 5821 5881 5881 6001 6061 Db Óγ g QΥ рp òγ g Ω qq Óγ QQ ΩÝ qq δy qq QY Db QΥ QC δy Dp Ω Db οy Dp QΥ QQ òγ q ργ Q Q gg δy

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8820 8880 8880 8940 9000 8280 8400 8580 8640 8640 8700 8700 8760 8760 8820 8280 8340 8400 8460 8460 8520 8520 8580 8100 8160 8160 8220 8220 8100 GCTTAGAGGGTGCCCAGGTCCTTCCATGGAGCCACTGGGGTTCCGGTGCACTAAAAAA CCTGAAGGAAGGTCCTGGAATGTGACTCCCTTGCTCCTTGTTGCTTTGGCATTCA GAAGGGGAACAGCAGAAAAAAAACAACCAACTGATCCTCAGCTGTCATTTCCTTTAAAAAGTC CCTGAAGGAAGGTCCTGGAATGTGACTCCCTTGCTCCTCTTGCTCTTTTGGCATTCA TTCTTTTTAAATGAAAAAGTAAGTAGGCCGGGCACGGTGGCTCACGCCTGTAATCCC TAACATGGTGAAACCCCATCTCAATAAAAATACAAAAATTAGCTGGGCGTGGTGGCAG CAGAGCTTGCAGTGAGCCGAGTTTGCGCCACTGCACTCCAGCCTAGGTGACAGAGTGAGA AGCACTTTGGGAGGCCAAAGCGGGTGGATCACGAGGTCAGGAGATCGAGACCATCCTGGC 8941 8761 8881 8461 8701 8761 8821 8821 8881 8341 8461 8521 8521 8581 8581 8641 8701 8161 8221 8281 8281 8341 8401 8401 8161 8221 7921 7981 7981 8041 8041 8101 8101 7861 7921 g g Q q q Db òγ Db QΥ g QΥ Qγ Db qq q Op Ω δ δy Q QY g Qγ g Qγ g δ ВÞ ò Db ò δy δý Ω

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O.Y	9001	AAAATCTAACCAGGACATTCAGGAATTGCTAGATTCTGGGAAATCAGTTCACCATGTTCA 9060 	
ΟŸ	90	GTCTTTTTTTTTTTGAGACTCTATTGCCCAGGCTGGAGTGCAATGGCATGAT 912	
Q	9061	ITTTTTTTTTTTTGAGACTCTATTGCCCCAGGCTGGAGTGCAATGGCAT	
Oy Dp	9121	CTGGGCTCACTGTAACCTCTGCCTCCCAGGTTCAAGCGATTCTCCTGTCTCAGCCTCCCA 9180	
Qy	9181	AGTAGCTGGGATTACAGGCGTGCACCACCATGCCCGGCTAATTTTTGTATTTTTAGTAGA 9240	
QY	9241	acagggtttcaccatgttggccaggctggtctcgaactctcctgacctcgtgatccg	
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Qy Db	9301	TGCCTCGGCCTCCCAAAGTGCTGACATTACAGGTGTGAGCCACCCTGCCCAGCCGTCAAA 9360 	
දු පු	9361	AGAGTCTTAATATATATATCCAGATGGCATGTGTTTACTTTATGTTACTACATGCACTTG 9420	
ò	2. 2	TGAAGGGCAGGTGCTTCAGGATACCATAT 948	
9	4	CTGCATAAATGTGGTACAAGCATTCTGTCTGAAGGGCAGGTGCTTCAGGATACCATAT 948	
QY Db	9481	ACAGCICAGAAGITICIICTITAGGCAITAAAITITAGCAAAGAIAICICAICTICIT 9540 	
Oy Dp	9541 9541	TTAAACCATTTTCTTTTTTTGGGTTAGAAAGTTATGTAGAAAAAGGTAAATGTGATTT 9600 	
QY	9601	ACGCTCATTGTAGAAAAGCTATAAAATGAATACAATTAAAGCTGTTATTTAATTAGCCAG 9660 	
Qy Db	9661 9661	TGAAAAACTATTAACAACTTGTCTATTACCTGTTAGTATTATTGTTGCATTAAAAATGCA 9720 	
Qy Db	9721	TATACTTTAATAAATGTATATTGTATAGGCATGATTTTATTGAAGTTCTTGTTC 9780 	
δy	78	84	
qq	9781	CTTGTGTATATACTTAATCGCTTTGTCATTTTGGAGACATTAATTTTGCTTCTAATT	
QY Db	9841	CTTTACATTTTGTCTTACGGAATATTTCATTCAACTGTGGTAGCCGAATTAATCGTGTT 9900 	
Qy	9901	CTTCACTCTAGGGACATTGTCGTCTAAGTTGTAAGACATTGGTTATTTTACCAGCAAA	
Q	9901		
Qy Dp	9961	CATTCTGAAAGCATATGACAAATTATTCTCTCTTAATATCTTACTATACTGAAAGCAGA 10020 	
Qy	10021	CTGCTATAAGGCTTCACTTACTCTACTCCATAAGGAATATGTTACAATTAATT	
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Unclassified.

Unclassified.

In (bases 1 to 10825)

RS Thomas, W.J., Drayna, D.T., Feder, J.N., Gnirke, A., Ruddy, D.,

Tsuchihashi, Z. and Wolff, R.K.

Method for determining the presence or absence of a hereditary, hemochromatosis gene mutation

NAL Patent: US 6228594-A 7 08-MAY-2001;

Location/Qualifiers

1. .10825

/Organism="unknown"
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                                                        GITAATTITITIAATAGAAATTITAAGTCCTCATTITCTTTCGGTGTTTTTAAGCTTAA
                                                                                                   TTTTTCTGGCTTTATTCATAAATTCTTAAGGTCAACTACATTTGAAAAATCAAAGACCTG
                                            CCAGTCTTCACAGTAACACATTTCACTAACACATTTACTAAACATCAGCAACTGTGGCCT
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Sequence 7 from patent US 6228594.
AR149462.1 GI:15114053
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BASE CO	OUNT 2999 a 2252 c 2648 g 2926 t
Query Best I Matche	y Match 100.0%; Score 10823; DB 6; Length 10825; Local Similarity 100.0%; Pred. No. 0; hes 10823; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy Db	1 TCTAAGGTTGAGATAAATTTTTAAATGTATGATTGATTTGAAAATCATAAATATTTA 60
Oy Dp	61 AATATCTAAAGTTCAGATCAGAACATTGCGAAGCTACTTTCCCCAATCAACAACACCCCT 120
0y 1 0b 1	121 TCAGGATTTAAAAACCAAGGGGACACTGGATCACCTAGTGTTTCACAAGCAGGTACCTT 180
Qy 1	181 CTGCTGTAGGAGAGGAGCTAAAGTTCTGAAAGACCTGTTGCTTTTCACCAGGAAGTT 240
Oy 2 Db 2	241 TTACTGGGCATCTCCTGAGCCAATAGCTGTAGGGTGACTTCTGGAGCCATCCCCG 300
9y 3	301 TTTCCCGCCCCCAAAAGAAGGGGAGATTTAACGGGGACGTGCGGCCAGAGCTGGGGAA 360
Oy 3	361 ATGGGCCGGGAGCCAGGCGGCGCTTCTCCTGATGCTTTTGCAGACCGCGGTCCTG 420
Oy Db	421 CAGGGGCGCTTGCTGCGTGAGTCCGAGGGCTGCGGCGAACTAGGGGCGGGGGGGG
oy da	481 GAAAAATCGAAACTAGTTTTCTTTGCGCTTGGGAGTTTGCTAACTTTGGAGGACCTGC 540
yo da	541 TCAACCCTATCGGAAGCCCTCTCCCTACTTTCTGCGTCCAGACCCCGTGAGGAGTGC 600
ò qa	601 CTACCACTGAACTGCAGATAGGGGTCCCTGGCCCCAGGACCTGCCCCCCCGGCTGT 660
o o	661 CCCGGCTCTGCGGAGTGACTTTTGGAACCGCCCACTCCCTTCCCCCACTAGAATGCTTT 720
λο q _Ω	721 TAAATAAATCTGGTAGTTGCTCACTTGAGCTGAGCTAAGCCTGGGGCTCCTTGAACCTGG 780
dg	781 AACTCGGGTTTATTTCCAATGTCAGCTGTGCAGTTTTTTCCCCAGTCATCTCCAAACAGG 840
oy Op	841 AAGTTCTTCCCTGAGTGCTTGCCGAGAAGCTGAGCAAACCCACAGCAGGATCCGCACGG 900
8 8	901 GGTTTCCACCTCAGAACGAATGCGTTGGGCGCGCGGAAAGAGTGCGTTGGGGA 960
οy	961 TCTGAATTCTTCACCATTCCACCCACTTTTGGTGAGACCTGGGGTGGAGGTCTCTAGGGT 1020

2040 2040 2100 1620 1680 1680 1740 1740 1800 1800 1860 1860 1920 1920 1980 1980 1200 1380 1440 1440 1500 1500 1560 1560 1620 1200 1260 1320 1320 1380 AATAAGAATGATATTGACTGGGAGCAGTATTTCCCAGGCAAACTGAGTGGGCCTGGCAAG CGCCTGGGGGTGGGAAGGGGACTACCATCTGCATGTAGGATGTCTAGCAGTATCCTGT AAATATTCATTGTTTACAAGTGTAAATGAGTCCCAGCCATGTGTTGCACTGTTCAAGCCC CTACGTGTATCCACATTTTACACATGACAAGAATGAGGCATGGCACGGCCTGCTTCCTGG 1501 CTACGIGIATCCACATITIACACAIGACAAGAAIGAGGCAIGGCAGGCCIGCITGCIGG TTTTCACTAGGCATAGGGAGGTAGGAGCTAATAATACGTTTATTTTACTAGAAGTTAACT TGTAGCACAGTGTTCTGTGGGTCACACGCCGGCCTCAGCACCACCACTTTGAGTTTTGGTA 1441 TGTAGCACAGTGTTCTGTGGGTCACACGCGGCCTCAGCACCACGCATTGGTA TAATGAACATGTAAGCAATGCACTCACTTCTAAGTTACATTCATATCTGATCTTATTTGA 1681 1741 1741 1801 1801 1861 1861 1921 1921 1981 2041 1441 1501 1681 1981 1141 1201 1261 1321 1021 1141 1201 1261 1321 961 1081 1081 1021 qq g QY QQ δy g ΩŸ pp δŽ Q Op οy Db Qy Db δ g δλ οp Oy Db οy g g qq QY Db οy g Qγ Ω QΥ Db QΥ δ Ω

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GCAGTA	AAAAATO	CGGGTTC	CGGGTT	CTCAGAZ	AGCCAAC	AGCCAAC	TGTGGAAAGCAGAATG	GAAAGC	AGTCCAC	TTGICIC	TTGTCT	GAGAAG	GAGAAG	CTGAGCTC	CTGAGC	ATACAA		AGGTGG	CTGTAC	CTGTAC	AAGAGT	AAGAGT	TGGCAA	TGGCAA	GATCTG	GATCTG	ACATAG	ACATAGO	AATCCC	AATCCC	NGCTTGG(NGCTTGG(
ATGTCTP	GACAACC	AGAAGCI	AGAAGCI	TAATGGG	GAATTCI		CTATGTG	CTATGIC	GTTACAC GTTACAC	CAAACCA	CAAACCA	AGAGAAA	AGAGAAA	CAGATTO	CAGATIC	ACAAAA		GAGGCTG	TGTGCCA	TGTGCC	AAAAGAC	AAAAGAG	GGGTAAT	GGGTAAT	AATCAAC	AATCAAC	TGAGGCC	TGAGGCC	CTTCTG	CTTCTG	GAGACA! GAGACA!
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GGGGTGC	ACTCACI	GCCACA	GCCACAT	AAGTAG1	ACAAGGI	ACAAGG	TCTGTCZ	TCTGTC	CAACAGI CAACAGI	GGAGTGC	GGAGTG	TGAAGG	TGAAGG	TAGTAGG	TAGTAG	ACCAGC 		GIGGIG	AGCCCA	AGCCCAC	ACAGAGO	ACAGAGO	GTTCTT	GTTCTT	ATGGTG	ATGGTG	TTAAGT	TTAAGT	AGAATTC	AGAATTO	CTGAGGC CTGAGGC
CGGCGTGGGGAAGGGGACTACCATCTGCATGTAGGATGTCTAGCAGTAT		AAACTTT	AAACTITGCCACATGTCACCTAGTAGACAAACTCCTGGTTAAGAAGGTCGGGTTGAAAA	AATAAACAAGTAGTGCTGGGAGTAQAGGCCAAGAAGTAGGTAATGGGCT 	GCCACAA	GCCACAA	ACAGTGATCTGTCACAGGCTTTTAAAAGATTGCTCTGGCTGCTAT	ACAGTGA	AGGGGGCAACAGTAAAAGCAGGAGCCCAGCCAGGAAGCTGTTAACACAGTCCAGGAAA 	AGGTAGT	AGGTAGT	TATATTC	TATATTC	CTGGGTGTAGTAGTCATGCCAAGGAGGAGGCCAAGGAGAGAGCAGATTCT'	cresers	GTTCAAGACCAGCCTGGGCAACACAGCAAAACCCTTCTCTACAAAAAATAAAAATTA GTTCAAGACCTGGGCAACACAGCAAAAACCTTCTTACAAAAAAAA		GCTGGGTGGGTGGCATGCACCTGTGATCCTACCTACTGGGGAGGCTGAGGTGGAGGTTACTGGAGGTTGAGTTGAGTTGAGTTGAGTTGAGTTGAGTTGAGTTGAGTTGAGTTGAGTTGAGTTGAGGTTACTGGAGGTTACTGAGTTGAGGTTAGTTGAGTTAGTTGAGTTGAGTTGAGTTGAGTTGAGTTGAGTTGAGTTGAGTTGAGTTGAGTTGAGTTGAGTTAGTTGAGTTGAGTTGAGTTGAGTTGAGTTGAGTTGAGTTGAGTTGAGTTGAGTTGAGTTGAGTTAGTTGAGGTTGAGTGAGGAG	TIGCTIG		CTAGGTG		TGACTTT	TGACTT	TTCTGAGATGGTGAAGGCAGAAGAGCAGTTTGGGGGTAAATCAAGGATCTGCATTTG	TTCTGAG	GGACATG	GGACATG	CAGTGTA	CAGTGTA	TTGGTGGCTGAGGCAGGTAGATCATTTGAGGTCAGGAGTTTGAGACAAGCTTGGCCAACA
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Qy Db	6541	. ATCACATTCAGCTGGGGATCAAGATAGCCTTCTGGATCTTGAAGGAGAGAGCTGGATTCCA 6600	
Qy	6601	TTAGGTGAGGTTGAAGATGATGGGGGGGTCTACACAGAGAGGAGCAACCATGCCAAGTAGGA 666	
Qy	6661	GAGTATAAGGCATACTGGGAGATTAGAAATTACTGTACCTTAACCCTGAGTTTGCGT 672 	
δŏ	7	AGCTATCACTCACCAATTATGCATTTCTACCCCTGAACATCTGTGGTGTAGGGAAAAGA 678	
0 7 E	6781	AGCTATCACTCACCAATTATGCATTTCTACCCCCTGAACATCTGTGGTGTGGGGAAAAGA 678 GAATCAGAAAGAAGCCAGCTCATACACAGTCCAAGGGTCTTTTGGGATATTGGGTTATGA 684	
OY.	4	TCACTGGGGGTGTCATGAAGGATCCTAAGAAGGAGGCCCACGATCTTTTGGGGTTGGGGGGGG	
qq	6841	TCACTGGGGTGTCATT	
QY Dp	6901	AATGTGTTGTTAAGAAGTTAGATGAGAGGTGAGGAGACCAGTTAGAAAGCCAATAAGCAT 6960 	
Oy Dp	6961	TICCAGAIGAGAGATAATGGITCIIGAAATCCAATAGIGCCCAGGICIAAAITGAGAIGG 7020 	
Qy Db	2 2	GTGAATGAGGAAAATAAGGAAGAGAGAGAGAGAGAGAGA	
Qy	7081	CTITCCTGGGTCTCTTGTCTCCACAGGAGGACCATGGGGCACTACGTCTTAGCTGAACG 7140	
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Qy	7201	TCAGGAGAGAGTTGAACCTAAACATAGAATT 726	
Qy	7261	CTCTGTTCATTTCCTCAAAAGATTTCCCCAT 732 	
Qy Db	7321	STTCCTGCATGCCGGTGATCCCTAGCTGTGACCTCTCCCCTGGAACTG 738	
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O.y D.b	7501 7501	ATTCATTTAACATCTGAGAAAGCTTTGAACCCTGGGACGTGGCTAGTCAT 756	

QY Db	7561 7561	AACCTTACCAGATTTTTACACATGTATCTATGCATTTTCTGGACCCGTTCAACTTTTCCT 7620
Qy Dp	7621 7621	TIGAAUCCTCTCTGTGTTACCCAGTAACTCATCTGTCACCAAGCCTTGGGGATTCTTC 7680
Qy	7681 7681	CATCTGATTGTGATGTGAGTTGCACAGCTATGAAGGCTGTACACTGCACGAATGGAAGAG 7740
Qy	7741	GCACCTGTCCCAGAAAAAGCATCATGGCTATCTGTGGGTAGTATGATGGTGTTTTTTAGC 7800
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Qy	7861	TIGCAAAGTITAATGGTGCCTTCATTTGGGATGCTACTCTAGTAT 7
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Qy	7981 7981	CTTCGTGTCCGACTCTTCTGAGCACCTACTTA 804
Qy	8041	ATAATTCTATGAGATAGGTACTATTATCCCCAT 81
Qy	8101	AAATGAAGAAAGTGAAGTAGGCCGGGCACGGTGGCTCACGCCTGTAATCCC 816
QY	8161 8161	CACTTTGGGAGGCCAAAGGGGTGGATCACGAGGTCAGGAGATCGAGACCATCCTGGC 822
Qy Db	8221 8221	TGAAACCCCATCTCTAATAAAAATACAAAAATTAGCTGGGCGTGGTGGCAG 828
Qy Dp	8281 8281	ATGAACCCAGGAGG 834 ATGAACCCAGGAGG 834
oy do	8341	GAGTTTGCGCCACTGCACTCCAGCCTAGGTGACAGAGTGAGA 840
Qy	8401	TCAAAAAAATAAAAATAAAAAAAAATGAAAAAAAAAAAA
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Qy Db	8521 8521	CTCAGACA CTCAGACA
Qy Db	8581	TCTTCTGAGTGAGCTTGAATCACAT 8.

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Qy Db	8701	CCTGAAGGAAGGTCCTGGAATGTGACTCCCTTGTTGTTGTTTTTTGGCATTCA, 8760
oy Oy	8761	TACGCAAGGACTGTA TACGCAAGGACTGTA
dy D	8821	TTCACACACGGTGTCCTCCCTAGGCCAGTGCCTCTGGAGTCAGAACTCTGGTGGTATTTC 8880
Oy Dp	8 8	CTCAATGAAGTGGAGTAAGCTCTCTCATTTTGAGATGGTATAATGGAAGCCACCAAGTG 894
QY Db	8941	GCTTAGAGGATGCCCAGGTCCTTCCATGGAGCCACTGGGGTTCCGGTGCACATTAAAAAA 9000
Qy Db	9001	
Qy Db	9061	AAAGACTCTTTTTTTTTTTGAGACTCTATTGCCCAGGCTGGAGTGCAATGGCATGAT 9120
Oy Dp	9121	CTCGGCTCACTGTAACCTCTGCCTCCCAGGTTCAAGCGATTCTCCTGTCTCAGCCTCCCA 9180
S q	9181 9181	AGTAGCTGGGATTACAGGCGTGCACCACCATGCCCGGCTAATTTTTGTATTTTTAGTAGA 9240
Qy Dp	9241	GACAGGGTTTCACCATGTTGGCCAGGCTGGTCTCGAACTCTCCTGACCTCGTGATCCGCC 9300
oy Dp	9301	GGCCTCCCAAAGTGCTGAGATTACAGGTGTGTGAGCCACCTG
6y Dp	9361	AGAGTCTTAATATATATATCCAGATGGCATGTGTTTACTTTATGTTACTGACATGCACTTG 9420
Oy Dp	9421	3TGGTACAAGCATTCTGTCTTGAAGGGCAGGT
Oy Dp	9481	SCTCAGAAGTTTCTTCTTTAGGCATTA
Qy Dp	9541 9541	TTAAACCATTTTCTTTTTTGTGGTTAGAAAGTTATGTAGAAAAAGTAAATGTGAATT 9600
Oy Db	9601	acgctcattgtagaaagctataaaatgaatacaattaaagctgttattaatta
Qy Db	9661	tgaaaaactattaacaacttgtctattacctgttagtattattgttgcattaaaatgca 9720
	9721	TATACTTTAATAAATGTATATTGTATTGTATACTGCATGATTTTATTGAAGTTCTTGTTC 9780

10741 CAGTATTTTATAAAACATTCTTCACAAACTCACACATTTAAAAACAAAACACTGTCTC 10800 10741 CAGTATTTTATAAAACATTCTTCACAAACTCACACACATTTAAAAACAAAACTGTCTC 10800 10440 10200 10200 10680 10140 10140 10260 10260 10560 0966 CATTCTGAAAGCATATGACAAATTATTTCTCTTAATATCTTACTATACTGAAAGCAGA TTTTTCTGGCTTTATTCATAAATTCTTAAGGTCAACTACATTTGAAAAATCAAAGACCTG CATITITAAATICITIAITCACCICIGGCAAAACCATICACAAACCAIGGIAGIAAAAGAGAA GGGTGACACCTGGTGGCCATAGGTAAATGTACCACGGTGGTCCGGTGACCAGAGATGCAG CTATTTGAATTGCTGGAATCACAGGCCATTGCTGAGCTGCCTGAACTGGGAACACACAG AAGGAAAACAAACCCACTCTGATAATCATTGAGTCAAGTACAGCAGGTGATTGAGGACTGC AGGTAAGCATTTGTTTTATATTGGTTTTTATTTCACCTGGGCTGAGATTTCAAGAAACACC TGAGAGGTACAGGCCAAAATTCTTATGTTGTATTATAATAATGTCATCTTATAATACTGT CTITACATITIGICITACGGAATATITICATICAACTGTGGTAGCCGAATTAATCGTGTT TAAAATCCCCAAATTTTTCATAAAC 10825 10501 10561 9901 10141 10201 10261 10321 10381 10441 10441 10501 10561 10621 10621 10681 10681 10801 9841 9841 9901 1966 1966 10021 10141 10201 10261 10321 10381 9721 9781 9781 10081 10021 10081 qq qq Dρ Db g ŏ g δλ g Q δy ōλ ŏλ ŏ δy qq δ g δ g οy g δ g δ g Ωÿ Ωp ò Q δý Dp οy δy ŏ

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Unclassified.
1 (bases 1 to 246240)
Feder,J.Nathan., Kronmal,G.Scott., Lauer,P.M., Ruddy,D.A.,
Fhomas,W., Tsucrithash1,?a and Wollff,R.K.
Megabase transcript map: novel sequences and antibodies thereto
Patent: US 5872237-A 20 16-FEB-1999;
Location/Qualifiers
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GTTTCCACCT	GGTTTCCACCTCAGAACGAATGCGTTGGCGGTGGGGCGCGAAAGAGTGGCGTTGGGGA 960
CTGAATTCTJ CTGAATTCTJ	
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TTTCACTAGG	
GAATTCAGAT 	TATATAACTCTTTTCAGGTTACAAGAACATAAATAATCTGGTTTTCTG 1380
TGTTATTTCA TGTTATTTCA	AGTACTACAGCTGCTTCTAATCTTAGTGACAGTGATTTTGCCCTGTAG 1440
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CTACGTGTATC(TATCCACATTTTACACATGACAAGAATGAGGCATGCCACGGCCTGCTTCCTGG 1560
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AAATATTCATTC 	CCCAGCCATGTTGCACTGTTCAAGCCC
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Db 196204 TCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGCAGCTGAGCTCAGAGTCTGAA 196263 196023 Db 195544 AIAGICCCAGGITITCAGGAGGCTIAGGIAGGAGAAICCCITGAACCCAGGAGGIGCAGG 195603 CTAGGTGACAGAGCAAGACCCTGTCTCCCTGACCCCTGAAAAAGAGAGAAGAGTTAAAGT 195183 195543 195663 195243 3840 3480 3420 ACCCAGGACTGTCATATGGAAGAAAGACAGGACTGCAACTCACCCTTCACAAAATGAGGA 3660 3180 3240 3060 CCAGACACAGCTGATGGTATGAGTTGATGCAGGTGTGTGGAGCCTCAACATCCTGCTCCC CCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCTTGTTTGAAGCTTTGGGCTA ATAGICCCAGGITITICAGGAGGCTTAGGIAGGAGAAICCCTIGAACCCAGGAGGIGCAGG CICCIACIACACATGGTTAAAGGCCTGTTGCTCTGTCTCCAGGTTCACACTCTGCACTA DD 195484 TGGTGAAACCCCATGTCTACTAAAATACAAAAATTAGCCTGGTGTGGTGGCGCACCCT TCTAATTTGCCCTGAGCACCAACTCCTGAGTTCAACTACCATGGCTAGACACACCTTAAC TGGTGAAACCCCCATGTCTACTAAAATAACAAAATTAGCCTGGTGGGGGGCGCACGCCT GGACATGTTAAGTTTGAGATTCCAGTCAGGCTTCCAAGTGGTGAGGCCACATAGGCAGTT CAGTGTAAGAATTCAGGACCAAGGCTGGGCACGGTGGCTCACTTCTGTAATCCCAGCACT TTGGTGGCTGAGGTAGATCATTTGAGGTCAGGAGTTTGAGACAAGCTTGGCCAACA TGACTTTGTTCTTTTTTTTTTTTTTTTGGCCTGAGCAGTGGGGTAATTGGCAATGCCAT TTCTGAGATGGTGAAGGCAGAAAGAAGAGCAGTTTGGGGTAAATCAAGGATCTGCATTTG 3721 3781 3481 195784 3601 195904 3661 3841 3421 195724 195964 Db 196024 Db 196084 196144 195364 3181 195124 2941 195244 3001 195304 3121 195424 3241 2881 195184 3061 g QQ qq οy g ŏλ Dp Qγ g δλ óλ δý Dp δλ ōλ οp g Op QQ g ŏ δλ ò δ δy δλ δy Qγ

99 3951 AGGTGGGARTCACANGTTCACTCTTCACCTTCTGCACTATTTTGCAAAATCACACACCACAG 19623 99 4021 CAAGGGTAATCACATGTTCACTTCTGACTTCTGCACTATTTTGCAAAATCACACACA
. 3961 196264 4021 196324 4081 196384 4141 196504 4321 196684 4381 196684 4381 19684 4501 19684 4501 19684 4501 19684 4621 19774 4621 19774

Qy	5041	GCCAAGATCGCGCCACTGCACTCCAGCCTAGGCAGCAGGAGTGAGACTCCATCATAAAAA	5100 197403
OY Db	5101	aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa	5160 197463
QQ QQ	5161	ATATCAAGTGAGGCCACTTATCAGAGTAGAATCCTTTAGGTTAAAAGTTTCTTTC	5220 197523
QV	5221	AGAACATAGCAATAATCACTGAAGCTACCTATCTTACAAGTCCGCTTCTTATAACAATGC	5280 197583
QQ Db	5281	CTCCTAGGTTGACCCAGGTGAAACTGACCATCTGTATTCAATCATTTTCAATGCACATAA [[[[[[[[]]]]]]]]]]]]]]]]]]]CTCCTAGGTTGACCAGGTGAACTGACATCTGTATTCAATCATTTTCAATGCACATAA	5340 197643
4a aa	5341	AGGGCAATTTTATCTATCAGAACAAAGAACATGGGTAACAGATATGTATTTACATGTG 	5400
Oy Dp	5401	AGGAGAACAAGCTGATCTGACTGCTCTCCAAGTGACACTGTGTTAGAGTCCAATCTTAGG	5460 197763
QY Db	5461	ACACAAAATGGTGTCTCCTGTAGCTTGTTTTTTCTGAAAAGGGTATTTCCTTCC	5520 197823
QV Db	5521	AACCTATAGAAGGAAGTGAAAGTTCCAGTCTTCCTGGCAAGGGTAAACAGATCCCCTCTC	5580 197883
QY Db	5581	CTCATCCTTCCTCTTTCCTGTCAAGTGCCTCCTTTGGTGAAGGTGACATCATGTGACCCTTTTTTTT	5640 197943
Qy	5641	TCTTCAGTGACCACTCTACGGTGTCGGGCCTTGAACTACTACCCCCAGAACATCACCCATG	5700 198003
Q7 Db	5701	AAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCTAAAGACGTATTG	5760 198063
QY	5761	CCCAATGGGGATGGGACCTACCAGGCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAG	5820 198123
QV	5821	CAGAGATATACGTNCCAGGTGGAGCACCCAGGATCAGCCCCTCATTGTGATCTGG	5880 198183
40 da	5881	GGTATGTGACTGATGAGAGCCAGGAGCTGAGAAATCTATTGGGGGTTGAGAGGAGTGCC 	5940 198243
QY	5941	TGAGGAGGTAATTATGGCAGTGAGATGAGGATCTGCTCTTTGTTAGGGGGTGGGCTGAGG 	6000 198303
QY	6001	GTGGCAATCAAAGCTTTAACTTGCTTTTTCTGTTTTAGAGCCCTCACCGTCTGGCACCC	6060 198363
QV Db	6061	TAGTCATTGGAGTCATCAGTGGAATTGCTGTTTTTGTCGTCATCTTGTTCATTGGAATTTTTTTT	6120 198423
δλ	6121	TGTTCATAATATTAAGGAAGAGGCAGGGTTCAAGTGAGTAGGAACAAGGGGGAAGTCTCT	6180

	GCATCCATGGG 6240	3AGACAGAAAAT 6300 	ACCIACIAI 6360 ACCIACIAI 198663		TTAAAGAAG 6480 TTAAAGAAG 198783	SAAAGAATG 6540 SAAAGAATG 198843	TGGATTCCA 6600		AGTITGCGT 6720 AGTITGCGT 199023	GGGAAAGA 6780 GGGAAAGA 199083	3GGTTATGA 6840 3GGTTATGA 199143	TATATGEG 6900 	AATAAGCAT 6960 AATAAGCAT 199263	TTGAGATGG 7020 TTGAGATGG 199323	GTGATGCCT 7080 GTGATGCCT 199383	AGCTGAACG 7140 AGCTGAACG 199443	ACTCAAAGA 7200 ACTCAAAGA 199503	ATAGAAATT 7260
	TAGTACCTCTGCCCAGGGCACAGTGGGAAGAGGGGCAGAGGGGATCTGG	AAGCATTTTCTCATTTATATTCTTTGGGGACACCAGCAGCAGCTCCCTGGGAGACA 	AATGGTTCTCCCCAGAATGAAAGTCTCTAATTCAACAACATCTTCAGAGCAC 	TTTGCAAGAGCTGTTTAAGGTAGTACAGGGGCTTTGAGGTTGAGAAGTCACTGTGGC 	TCTCAGAACCCAAATCTGGTAGGGAATGAAATTGATAGCAAGTAAATGTAGTTAAAGAAG 	ACCCCATGAGGTCCTAAAGCAGGCAGGAAGCAAATGCTTAGGGTGTCAAAGGAAAGAAT 	ATCACATTCAGCTGGGGATCAAGATAGCCTTCTGGATCTTGAAGGAGAAGCTGG 	TTAGGTGAGGTTGAAGATGATGGGAGGTCTACACACAGACGAGCAAG 	GAGTATAAGGCATACTGGGAGATTAGAAATAATTACTGTACCTTAACCCTGAGTTTG 	AGCTATCACTCACCAATTATGCATTTCTACCCCCTGAACATCTGTGGTGTAGGG.	GAATCAGAAAGAAGCCAGCTCATACAGAGTCCAAGGGTCTTTTGGGATATTGGG' 	TCACTGGGGTGTCATTGAAGGATCCTAAGAAGGAGGACCACGATCTCCCTTATATGGT. [AATGTGTTGTTAAGAAGTTAGATGAGGGGGGGGCACCAGTTAGAAAGCCAATAAGCAT 	TTCCAGATGAGATAATGGTTCTTGAAATCCAATAGTGCCCAGGTCTAAATTGAGAT/ 	GTGAATGAGGAAAATAAGGAAGAGAGAGAGAGGCAAGATGGTGCCTAGGTTTTC	CTTTCCTGGGTCTCTTGTCTCCACAGGAGGCCATGGGGCACTACGTCTTAGCTC	TGAGTGACACGCAGCCTGCAGACTCACTGTGGGAAGAGAGAAAAAAAA	GGGAGTGCATTTATGAGCTCTTCATGTTTCAGGAGAGAGGTTGAACCTAAAACTTAGAAATT
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qq	199504	GGGAGTGCATTTATGAGCTCTTCATGTTTCAGGAGAGAGTTGAACCTAAACATAGAAATT	199563
Qy Db	7261	GCCTGACGAACTCCTTGATTTTAGCCTTCTGTTCATTTCCTCAAAAAGATTTCCCCAT	7320 199623
QV da	7321	TTAGGTTTCTGAGTTCCTGCATGCCGGTGATCCCTAGCTGTGACCTCTCCCCTGGAACTG	7380 199683
Qy Db	7381	TCTCTCATGAACCTCAAGCTGCATCTAGAGGCTTCCTTCATTTCCTCGTCACCTCAGAG	7440 199743
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oy Db	7501	CTTACATGATTCATTTTAACATCTGAGAAAAGCTTTGAACCCTGGGACGTGGCTAGTCAT 	7560 199863
Qy Db	7561	AACCTTACCAGATTTTTACACATGTATCTATGCATTTTCTGGACCGGTCAACTTTTCCT	7620 199923
Qy Db	7621	TTGAATCCTCTCTCTGTGTTACCCAGTAACTCATCTGTCACCAAGCCTTGGGGATTCTTC	7680 199983
, Qy da	7681	CATCTGATTGTGATGTGAGTTGCACAGCTATGAAGGCTGTACACTGCACGAATGGAAGGGCGTGTACACTGCACGAATGGAAGAGCTGTACACTGCACGAATGGAAGAGCTGTACACTGCACGAATGGAAGAG	7740 200043
Q qq	7741	GCACCTGTCCCAGAAAAGCATCATGGCTATCTGTGGGTAGTATGATGGTGTTTTTTAGC	7800 200103
Q Q	7801	AGGTAGGAGGCAAATAICTIGAAAGGGTIGIGAAGAGGTGTITITITITITATIGGCAIGA 	7860 200163
Qy Db	7861	AGGTGTCATACAGATTTGCAAAGTTTAATGGTGCCTTCATTTGGGATGCTACTCTAGTAT	7920 200223
Qy Dp	7921	TCCAGACCTGAAGAATCACAATAATTTTCFACCTGGTCTCTCCTTGTTCTGAFAAAA 	7980 200283
Qy	7981	ATTATGATAAGGATGATAAAAGCACTTACTTCGTGTCCGACTCTTCTGAGCACCTACTTA	8040 200343
Qy	8041	CATGCATTACTGCATGCACTTCTTACAATAATTCTATGAGATAGGTACTATTATCCCCAT	8100 200403
Qy Db	8101	TICITITITAAAIGAAAAAGAGAAGAGAAGACCGGGCACGGIGGCTCACGCCTGIAATCCC 	8160 200463
oy da	, 8161) 200464	AGCACTITGGGAGGCCAAAGGGGGTGGATCACGAGGTCAGGAGATCGAGACATCCTGGC	8220 200523
qa ap	8221	TAACATGGTGAAACCCCATCTCTAATAAAATACAAAAATTAGCTGGGCGTGGTGGCGG 	8280 200583
Qy Db	8281	ACGCCTGTAGTCCCAGCTACTCGGAAGGCTGAGGAGAAATGGCATGAACCCAGGAGG 	8340 200643

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644 CAGAGCTIGCAGTGAGTGAGTGAGTGAGTGAGCTAGGTGAGTGAGTGA	400 00703
8401 CTCCATCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	460 00763
8461 TAGAGTATCTCATAGTTTGTCAGTGATAGAAACAGGTTTCAAACTCAGTCAATCTGACCG 8: 	520 00823 `
8521 TTTGATACATCTCAGACACCACTACATTCAGTAGTTTAGATGCCTAGAATAAATA	580 00883
8581 GGAAGGAGGTCTTTTTTTTTCTCATTGTGTTTCTTCTGAGTGAG	640 00943
8641 GAAGGGGAACAGCAGAAACAACCAACTGATCCTCAGCTGTCATGTTTCCTTTAAAAGTC 87 	700 01003
8701 CCTGAAGGAAGGTCCTGGAATGTGACTCCCTTGCTCCTCTGTTGCTCTTTTGGCATTCA 8701004 CCTGAAGGAAGGTCCTGGAATGTGACCTTGCTCCTTGTTGCTCTTTGGCATTCA 20	760 01063
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8821 TTCACACACAGTGTCCTCCCTAGGCCAGTGCCTCTGGAGTCAGAACTCTGGTGGTATTTC 86	880 01183
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9181 AGTAGCTGGGATTACAGGCGTGCACCACCAGGCCGGCTAATTTTGTATTTTAGTAGA 92	240 01543
9241 GACAGGGTTCACCATGTTGGCCAGGCTGGTCTCGAACTCTCCTGACCTCGTGATCCGCC 93	300 01603
9301 TGCCTCGGCCTCCCAAAGTGCTGAGATTACAGGTGTGAGCCACCCTGCCCAGCCGTCAAA 93 	360 01663
9361 ACAGTCTTAATATATATATCCAGATGGCATGTGTTTACTTTATGTTACTACATGCACTTG 94 	420 01723

201903 201783 201843 202143 202263 202443 202743 202023 202203 202383 10200 202503 202083 10020 10080 10140 10260 10320 CATITITAAATITCITATITCACCICIGGCAAAACCATITCACAAACCATGGTAGTAAAGAGAA 10380 202683 202803 10500 0996 9720 9780 9840 0066 0966 10501 ATCACTIGIAGAGAAAAGCCCCTGAAAATTIGAGAAAACAAAGAAACAAGAAACTACTIACCAG 10560 GCTGCATAAATGTGGTACAAGCATTCTGTCTTGAAGGGCAGGTGCTTCAGGATACCATAT 201844 TTAAACCATTTTCTTTTTTTTGGTTAGAAAGTTATGTAGAAAAAGTAAATGTGATTT ACAGCTCAGAAGTTTCTTCTTTAGGCATTAAAATTTTAGCAAAGATATCTCATCTTCTT ACGCTCATTGTAGAAAAGCTATAAAATGAATACAATTAAAAGCTGTTATTTAATTAGCCAG CATTCTGAAAGCATATGACAAATTATTTCTCTTTAATATCTTACTATACTGAAAGCAGA TITITCTGGCTTTATTCATAAATTCTTAAGGTCAACTACATTTGAAAAATCAAAGACCTG CGCTGAGGGTTTTCCTGAAGGTAAAGGAATAAAGAATGGGTGGAGGGGGGTGCACTGGAA TTAAACCATTTTCTTTTTTGTGGTTAGAAAGTTATGTAGAAAAAAAGTAAATGTGATTT CTTTACATTTTGTCTTACGGAATATTTTCATTCAACTGTGGTAGCCGAATTAATCGTGTT TCTTCACTCTAGGGACATTGTCGTCTAAGTTGTAAGACATTGGTTATTTTACCAGCAAAC CCAGICITCACAGIAACACAITICACIAACACAITIACIAAACAICAGCAACIGIGGCCI GITAATTTTTAATAGAAATTTTAAGICCTCATTTTCTTTCGGTGTTTTTAAGCTTAA CGCTGAGGGTTTTCCTGAAGGTAAAGGAATAAAGAATGGGTGGAGGGGCGTGCACTGGAA 9481 9541 9601 1996 9841 9961 9421 201784 201904 201964 9781 202084 10261 201724 202144 9901 202264 202324 10081 202384 10141 202444 202624 202684 10441 202744 202204 10021 10201 202504 202564 10321 10381 q g g pp Qy В δy δλ ΟŊ δλ Óγ ρp Qγ a οy QΥ δŏ Qγ qq δy qq δy g Qγ Dp qq δy g δλ qq qq Q Qγ οp Qγ g δλ

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                                                                                     AAGGAAAACAAACCACTCTGATAATCATTGAGTCAAGTACAGCAGGTGATTGAGGACTGC
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Feder,J.Nathan., Kronmal,G.Scott., Lauer,P.M., Ruddy,D.A., Thomas,W., Tsuchlhashl,Z. and Wolff,R.K.
Megabase transcript map: novel sequences and antibodies the Patent: US 587237-A 21 16 FEB-1999;
Location/Qualifiers
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                                    CTATTTGAATTGCTGGAATCACAGGCCATTGCTGAGCTGCCTGAACTGGGAACACAG
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193444 CTAGGCTTTATTGATTTGCAATGTGCTGTGAATTAAGAGGCCTCTCTACAAAGTACTGA 193503
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                         Db 192664 ATGGGCCCGCGAGCCAGGCCGCCTTCTCTCTCTCTGTTTTGCAGACCGCGTCCTG
                                                                 GAAAAATCGAAACTAGCTTTTCTTTGCGCTTGGGAGTTTGCTAAACTTTGGAGGACCTGC
                                                                                                                                                                           Db 192844 TCAACCCTATCCGCAAGCCCCTCTCCCTACTTTCTGCGTCCAGACCCCGTGAGGGAGTGC
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                                                   CAGGGGCGCTTGCTGCGTGAGTCCGAGGCTGCGGGCGAACTAGGGGCGCGCGGGGGTG
                                                                                                         GAAAAATCGAAACTAGCTTTTTCTTTGCGCTTGGGAGTTTGCTAACTTTGGAGGACCTGC
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195243 195003 195543 195843 195063 195183 195303 195483 195603 195663 195723 2940 3120 2820 3180 3240 3300 3360 3480 3540 3420 ACCCAGGACTGTCATATGGAAGAAAGACAGGACTGCAACTCACCTTCACAAAATGAGGA 3660 195244 TTCTGAGATGGTGAAGGCAGAGGAAAGAGCAGTTTGGGGTAAATCAAGGATCTGCATTTG GCTGGGTGTGGTGGCATGCACCTGTGATCCTAGCTACTCGGGAGGCTGAGGTGCAGGGTA TGACTITGTTCTTTATTTTATTGGCCTGAGCAGTGGGGTAATTGGCAATGCCAT TTCTGAGATGGTGAAGGCAGAAAGAAGGAGTTTGGGGTAAATCAAGGATCTGCATTTG CAGTGTAAGAATTCAGGACCAAGGCTGGGCACGGTGGCTCACTTCTGTAATCCCAGCACT TTGGTGGCTGAGGCAGGTAGATCATTTGAGGTCAGGAGTTTGAGACAAGCTTGGCCAACA CTGGGGGCAGTGAGGGGGTGGCCACGTGTGGCCAGAGAAAAGCACACAAGGAAAGAGC CTGGGTGTAGTAGCTCATGCCAAGGAGGAGGCCAAGGAGAGCAGATTCCTGAGCTCAGGA GTTCAAGACCAGCCTGGGCAACACAGCAAAACCCCTTCTCTACAAAAATACAAAAATTA TTGCTTGAGCCCAGGAAGTTGAGGCTGCAGTGAGCCATGAGCTGTGCCACTGTACTTCAGC ATAGTCCCAGGTTTTCAGGAGGCTTAGGTAGGAGAATCCCTTGAACCCAGGAGGTGCAGG CTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAACTGAAGGAATTATTCCTCAGGATTTGGG ATTITCTAGAATCCACCAGCTTTAGTGGAGTCTGTCTAATCATGAGTATTGGAATAGGAT GCACATGTTAAGTTTGAGATTCCAGTCAGGCTTCCAAGTGGTGAGGCCACATAGGCAGTT TTGCAGTGAGCTGAGATTGTGCCACTGCACTCCAGCCTGGGTGATAGAGTGAGACTCTGT TCTAATTTGCCCTGAGCACCAACTCCTGAGTTCAACTACCATGGCTAGACACACCTTAAC 2641 2701 2761 2881 2941 3061 3121 3181 3301 3421 3481 3541 2581 194944 195064 2821 195184 3001 195304 3241 195544 195724 194824 194884 195004 195124 195364 195424 195484 195604 3361 195664 195844 3601 195784 g g ŏλ qq δy qq qq ŏ g Pp δλ g g δý g δλ g qq qq q g QΩ δy δ δ δλ Qγ δy οy δ QΥ δŽ QQ δ QQ δy

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à d	3661	CCAGACACAGGTGATGGTATGAGTTGATGCAGGTGTGGGGGCCTCAACATCCTGCTCCC 3720	
oy d	3721	TCCTACTACACATGGTTAAGGCCTGTTGCTCTGTGTCTCCAGGTTCACACTCTGCACTA 3	
oy Dp	378.	CTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCTTGTTTGAAGCTTTGGGCTA 3840	
S S	3841	CGTGGATGACCAGCTGTTCGTGTTCTATGATNATGAGAGTCGCCGTGTGGAGCCCCGAAC 3900 	
oy G	3901	TCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGCAGCTGAGTCAGAGTCTGAA 3960 	
5 G	396	GGGTGGGATCACAGTTCACTGTTGACTTCTGGACTATTATGGAAATCACAACCACAG 4020 	
9 P	4021	SCCTCACCTTCCTGAGGTTGTCAG	
oy Op	4081	ATGCATCTTGAAGGAAACAGCTGGAAGTCTGAGGTCTTGTGGGAGGAGGGAAGGAGGAAG 4140 	
oy Op	4141	GAATTTGCTTCCTGAGATCATTTGGTCCTTGGGGATGGTGGAAATAGGGACCTATTCCTT 4200 	
OY Db	4201	IGGTIGCAGTIAACAAGGCIGGGGATITITCCAGAGICCCACACCCTGCAGGICAICCTG 4260 	
Qy Db	4261	GGCTGTGAAATGCAAGAAGAACAACAGTACCGAGGGCTACTGGAAGTACGGGTATGATGGG 4320 	
oy B	4321	CAGGACCACCTIGAATICTGCCCTGACACTGGATTGGAGAGCAGCAGCAGAGCCCAGGGCC 4380 	
Oy Dp	4381	TGGCCCACCAAGCTGGAGAGAAGCACAAGATTCGGGCCAGGAGAACAGGGCCTAC 4440 	
9 9	4441	CTGGAGAGGGACTGCCCTGCACCTGCAGCAGTTGCTGGAGCTGGGGAGAGGTGTTTTG 4500 	
0 <u>y</u>	4501 196804	GACCAACAAGGTATGGTGGAAACACACTTCTGCCCCTATACTCTAGTGGCAGAGTGGAGG 4560 	
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Oy Op	4621 196924	TCCAAATTCTGGGAAGGGACTTTCTCAATCCTAGAGTCTCTACCTTATAATTGAGATGTA 4680 	
QO.	4681	TGAGACAGCCACAAGTCATGGGTTTAATTTCTTCCATGCATATGGCTCAAGGGAA 4740 	

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	CTCATCCTTCCTCTTTCCTGTCAAGTGCCTCCTTTGGTGAAGGTGACACATCATGTGACC	5581	Qy
	AACCTATAGAAGGAAGTGAAAGTTCCAGTCTTCCTGGCAAGGTAAACAGATCCCTCTC	5521 197824	QY Dp
197823	ACACAAAATGGTGTCTCCTCTTGTAGCTTGTTTTTTTTTT	197764	QO
	ACACAAAATGGTGTCTCTCTGTAGCTTGTTTTTTCTGAAAAGGGTATTTCCTTCC	5461	ΟŊ
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	AGGAGAACAAGCTGATGCTGCTCTCCAAGTGACACTGTGTTAGAGTCCAATCTTAGG	5401	Qy
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	CICCTAGGITGACCAGGIGAAACIGACCATCTGTATTCAATCTTTCAATGACATAAA	197584	S G
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197523	ATATCARGIGAGCCCACTTATCAGGGTAGAGGATCCTTTAGGTTAAAAGTTCTTCAT	197464	S G
197	AAAAAAAAAAAAAAAAGAGAATTCAGAGATCTCAGGTATCATATGAATA	197404	QQ
Ŋ		5101	ΟY
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510	GCCAAGATCGCGCCACTGCACTCCAGCCTAGGCAGAGAGTGAGACTCCATCATAAAAAA	5041	Qy
197343	GCTAATTGGAAGGCTGAGGCAGGAGCATCGCTTGAACTTGGAAGCGGAAGCTGCACTGA	197284	qq
504	GCTAATTGGAAGGCTGAGGCAGGAGCATCGCTTGAACCTGGGAAGCGGAAGTTGCACTGA	4981	δλ
197		7	Db
4980	ACCCGTCTCTAAAAAAAAAAAAATTAGCTGGTCACAGTCATGCGCACCTGTAGTC	4921	QΥ
97	AGGCCGAG	197164	qq
4920	AGGCCGAGGCGGGTGCTCACAAGGTCAGGAGTTTGAGACCAGCCTGACCAACATGGT	4861	QY
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. 1 CAGAGATATACGTNCCAGGTGGAGCACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGG 5	1 GGTATGTGACTGACAGGAGCAGGAGCTGAGAAATCTATTGGGGGTTGAGAGGAGTGC 5	1 TGAGGAGGTAATTATGGCAGTGAGATGAGGATCTGCTCTTTGTTAGGGGGTGGGCTGAGG 6	1 GIGGCAATCAAAGGCTTTAACTTGCTTTTTGTCTTTTAGAGCCCTCACCGTCTGGCACC 6	1 TAGTCATTGGAGTCATCAGTGGAATTGCTGTTTTTGTCGTCATCTTGTTCATTGGAATTT 6	1 TGTTCATAATATTAAGGAAGAGGCAGGGTTCAAGTGAGTAGGAACAAGGGGGAAGTCTCT 6	1 TAGTACCTCTGCCCCAGGGCACAGTGGGAAGAGGGGCAGAGGGGATCTGCCATCCTGGG 6	1 AAGCATTTTTCTCATTTATATTCTTTGGGACACCAGCAGCTCCCTGGGAGACAGAAAT 6	1 AATGGTTCTCCCCAGAATGAAAGTCTCTAATTCAACAACAACATCTTCACAGCACCTACTAT 6	1 TTGCAAGAGCTGTTTAAGGTAGTACAGGGGCTTTGAGGTTGACAAGTCACTGTGGCTAT 6	1 TCTCAGAACCCAAATCTGGTAGGGAATGAATTGATAGCAAGTAAATGTAGTTAAAGAA 6	1 ACCCCATGAGGTCCTAAAGCAGGCAGGAAGCAATGCTTAGGGTGTCAAAGGAAAGAATG 6	1 ATCACATTCAGCTGGGGATCAAGATAGCCTTCTGGATCTTGAAGGAGAAGCTGGATTCCA 6	1 TTAGGTGAGGTTGAAGATGATGGGAGGTCTACACAGACGAGCAGCAACCATGCCAAGTAGGA 6 1111111111111111111111111111111111	1 GAGTATAAGGCATACTGGGAGATTAGAAATAATTACTGTACCTTAACCCTGAGTTTGCGT 6	AGCTATCACCACCAATTATGCATTTCTACCCCCTGAACATCTGTGGGGTGTAGGGAAAAGA 6	GAATCAGAAAGAAGCCAGCTCATACAGAGTCCAAGGGTCTTTTGGGATATTGGGTTATGA 6	1 TCACTGGGGTGTCATTGAAGGATCCTAAGAAAGGAGGACCACGATCTCCCTTATATGGTG 6	1 AAFGFGTTGTTAAGAAGTTAGATGAGGTGAGGAGACCAGTTAGAAAGCCAATAAGCAT 6
Qy 5821	QY 5881	Qy 5941	Qy 6001	Qy 6061	Oy 6121	Qy 6181	Qy 6241	Qy 6301	Qy 6361	y 642;	Qy 6481	Oy 6541	Qy 6601	Qy 6661	Qy 6721	Oy 6781	Oy 6841	Qy 6901
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200044 GCACCTGTCCCAGAAAAGCATCATGATCTGTGGGGTAGATGATGGTGTTTTTAGC 200103 199323 199324 GTGAATGAGGAAAATAAGGAAGAGAGAAGAGGCAAGATGGTGCCTAGGTTTGTGATGCCT 199383 199504 GGGAGTGCATTTATGAGCTCTTCATGTTTCAGGAGAGAGTTGAACCTAAACATAGAATT 199563 199684 TCTCTCATGAACCTCAAGCTGCATCTAGAGGCTTCCTTCATTTCCTCCCGTCACCTCAGAG 199743 199803 199863 199923 199983 200043 200163 200233 200224 TCCAGACCTGAAGAATACACAATAATTTTCTACCTGGTCTCTCCTTGTTCTGATAATGAAA 200283 7680 7740 7140 7320 8040 7560 7860 7500 199864 AACCTTACCAGATTTTTACACATGTATCTATGCATTTTCTGGACCCGTTCAACTTTCCT CTTTCCTGGGTCTCTTGTCTCCACAGGAGCACTGGGGGCACTACGTCTTAGCTGAACG GCCTGACGAACTCCTTGATTTTAGCCTTCTCTGTTCATTTCCTCAAAAAGATTTCCCCAT TTAGGTTTCTGAGTTCCTGCATGCCGGTGATCCCTAGCTGTGACCTCTCCCCTGGAACTG ACATACACCTATGTCATTTCATTTCCTATTTTGGAAGAGGACTCCTTAAATTTGGGGGA TTGAATCCTCTCTCTGTGTTACCCAGTAACTCATGTGTCACCAAGCCTTGGGGGATTCTTC AGGTGTCATACAGATTTGCAAAGTTTAATGGTGCCTTCATTTGGGATGCTACTCTAGTAT TCCAGACCTGAAGAATCACAATAATTTTCTACCTGGTCTCTCCTTGTTCTGATAATGAAA TGAGTGACACGCAGCCTGCAGACTCACTGTGGGAAGGAGACAAAACTAGAGACTCAAAGA TCTCTCATGAACCTCAAGCTGCATCTAGAGGCTTCCTTCATTTCCTCCGTCACCTCAGAG CITACATGATTCATTTAACATCTGAGAAAAGCTTTGAACCCTGGGACGTGGCTAGTCAT GCACCTGTCCCAGAAAAAGCATCATGGCTATCTGTGGGTAGTATGATGGGTGTTTTTAGC CTTTCCTGGGTCTCTTGTCTCCACAGGAGGAGCCATGGGGCCACTACGTCTTAGCTGAACG GGGAGTGCATTTATGAGCTCTTCATGTTTCAGGAGAGAGTTGAACCTAAAAATT **AACCTTACCAGATTTTTACACATGTATCTATGCATTTTTCTGGACCCGTTCAACTTTTCCT** GTGAATGAGGAAAATAAGGAAGAGAGAGAGAGGCAAGATGGTGCCTAGGTTTGTGATGCCT 7741 7081 7141 7381 7441 7501 7561 7861 7921 1969 199384 199444 7201 7261 199564 199624 199744 199804 7621 199924 7801 200104 200164 7981 199204 199264 7021 7321 g δŏ qq gg QΥ g δŏ g Пр δŏ Б ò g qq ΩŸ Ωp δŏ g ò qq ò g QΥ g δλ g δ g δ Dp g ŏ Qγ ōλ δ ÓΥ

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1 CAT	CATGCATTACTGCATGCACTTCTTACAATAATTCTATGAGATAGGTACTATTATCCCCAT 8100
01 TT(04 TT(TTCTTTTTAAATGAAGAAAGTGAAGTAGGCCGGGCACGTGGCTCACGCCTGTAATCCC 8160
61 AG 64 AG	AGCACTITGGGAGGCCAAAGCGGGTGGATCACGAGGTCAGGACATCGAGACCATCCTGGC 8220
1 TA 	TAACATGGTGAAACCCCATCTCTAATAAAAATACAAAAATTAGCTGGGGGTGGTGGCAG 8280
1 AC	ACGCCTGTAGTCCCCAGCTACTCGGAAGGCTGAGGAGAATGGCATGAACCCAGGAGG 8340
1 4 2 _ 2	CAGAGCTTGCAGTGAGCCGAGTTTGCGCCACTGCAGCCTAGCTGACAGAGTGAGA 8400
01 04 02 03	ctccatctcaaaaaataaaaataaaaataaaaaaaaagaaaaaaaa
61 Ti 64 Ti	TAGAGTATCTCATAGTTTGTCAGTGATAGAAACAGGTTTCAAACTCAGTCAATCTGACCG 8520
21 T	TTTGATACATCTCAGACACCACTACATTCAGTAGTTTAGATGCCTAGAATAAATA
8581 G 1 00884 G	GGAAGGAGATGGCTCTTCTCTTGTCTCATTGTGTTTCTTCTGAGTGAG
8641 G 00944 G	GAAGGGGAACAGCAAAAACAACCAACTGATCCTCAGCTGTCTCCTTTAAAAGTC 8700
8701 C 01004 C	CCTGAAGGAAGGACCTGGAATGTGACTCCCTTGTTGTTGTTTTTGGCATTCA 8760
8761 T 01064 T	TTTCTTTGGACCCTACGCAAGGACTGTAATTGGTGGGGACAGCTAGTGGCCCTGCTGGGC 8820
8821 T 201124 T	TTCACACACGGTGTCCTCCCTAGGCCAGTGCCTCTGGAGTCAGAACTCTGGTGGTATTC 8880
8881 C	CCTCAATGAAGTGGAGTAAGCTCTCTCATTTTGAGATGGTATAATGGAAGCCACCAGGTG 8940
41 (GCTIAGAGGATGCCCAGGTCCTTCCATGGAGCCACTGGGGTTCCGGTGCACATTAAAAAA 9000
01 7	aaaatctaaccaggacattcaggaattgctagattctgggaaatcagttcaccatgttca 9060
9061 7	AAAGAGTCTTTTTTTTTTTGAGACTCTATTGCCCAGGCTGGAGTGCAATGGCATGAT 9120

202323 202503 20203 202203 202263 201783 201843 201903 201963 202083 202143 10200 201723 10020 10080 201603 9840 0066 0966 9540 0996 9720 9780 9240 201964 TGAAAAACTATTAACAACTTGTCTATTACCTGTTAGTATTATTGTTGCTGATAAAATGCA 202024 TATACTTTAATAAATGTATATGTATTGTATACTGCATGATTTATTGAAGTTCTTGTTC 202144 CITTACATITIGECTTACGGAATATITICATICAACTGTGGTAGCCGAATTAACTIT CCAGTCTTCACAGTAACACATTTCACTAACACATTTACTAAACATCAGCAACTGTGGCCCT TGAAAAACTATTAACAACTTGTCTATTACCTGTTAGTATTATTGTTGCATTAAAAATGCA TATACTTTAATAATGTATATTGTATTGTATACTGCATGATTTTATTGAAGTTCTTGTTC 202084 ATCTTGTGTATATACTTAATGCTTTGTCATTTTGGAGACATTATTTGCTTCTAATTT 9841 CTTTACATTTTGTCTTACGGAATATTTTCATTCAACTGTGGTAGCCGAATTAATCGTGTT GCTGCATAAATGTGGTACAAGCATTCTGTCTTGAAGGGCAGGTGCTTCAGGATACCATAT 201724 GCTGCATAAATGTGGTACAAGCATTCTGTCTTGAAGGGCAGGTGCTTCAGGATACCATAT ACAGCTCAGAAGTTTCTTTTAGGCATTAAATTTTAGCAAAGATATCTCATCTTTTTTT AGAGTCTTAATATATATATCCAGATGGCATGTGTTTACTTTATGTTACTACATGCACTTG 9721 9781 9961 202264 202324 10081 202384 10141 202444 9541 9661 10021 9421 9481 9301 201664 201784 201844 9121 9241 201604 9361 201424 9181 201544 201484 δλ g Οy g QC q g δ QQ g g ò Qγ Ω qq pp g δy g g ōλ δ δ Op δ ò Dp δy qq QΫ g QΫ́ Qγ ŏ Ω

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Feder, J. Nathan., Kronmal, G. Scott., Lauer, Thomas, W., Tsuchihashi, Z. and Wollf, R.K. Megabase transcript map: novel sequences Patent: US 5872237-A 22 16-FFB-1999;
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3060	GGACATGTTAAGTTTGAGATTCCAGTCAGGCTTCCAAGTGGTGAGGCCACATAGGCAGTT	30	Qy
3000	TTCTGAGATGGTGAAGGCAGAGGAAAGACA	2941	Qy
195303		195244	Db
2940	TGACTTTGTTCTTTATTTTAATTT	2881	QY
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2880	CTAGGTGACAGAGCAGAGCCTGTCTCCCTGACCCCTGAAAAAGAAGAAGAGTTAAAGT	2821	Qy
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2760	GCTGGGTGTGGTGGCATGCACCTGTGATCCTAGCT	2701	Qy
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2640	CTGGGTGTAGTAGCTCATGCCAAGGAGGCCAAGGAGAGCAGATTCCTGAGCTCAGGA	2581	Qy
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2580	TATATTCTGAAGGAAGTTGCTGAAGGATTCTATGTTGTGTGAGAGAAAGAGAAATTGG	2521	Qy
194883		194824	Dp
2520	AGGTAGTGGAGTGGGCTGGGTAGCAAAAGGGAGTGACAAACCATTGTCTCCTGAA	2461	Oy
194823		194764	Dp
2460	AAGGGAGCAACAGTAAAAGCAGGGAGCCCAGCCAGGAAGCTGTTACACAGTCCAGGCAAG	2401	Qy
194763		194704	Dp
2400	ACAGTGATCTGTCACAGGCTTTTAAAAGATTGCTCTGGCTGCTATGTGGAAAGCAGAATG	2341	Oy
194703			Db
2340	GCCACAAACAAGGTTGTGCAGGCGCCTGTAGGCTGTGGTGTGAATTCTAGCCAAGGAGTA	2281	QY
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QQ	199984	CATCTGATTGTGATGTGTGTTGCACAGCTATGAAGGCTGTACACTGCACGAATGGAAGGG 2(00043
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Db			00103
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Db			00223
Qy	7921	TCCAGACCTGAAGAATCACAATAATTTTCTACCTGGTCTCTCCTTGTTCTGATAATGAAA 79	980
Db			00283
O _Y	7981	ATTATGATAAGGATGATAAAAGCACTTACTTCGTGTCCGACTCTTCTGAGCACCTACTTA 8(040 00343
Qy	8041	CATGCATTACTGCATGCACTTCTTACAATAATTCTATGAGATAGGTACTATTATCCCCAT 81	8100
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Db			200703
Qy Db	8401	CTCCATCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	460 00763
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QY	8521 200824	TITGATACATCTCAGACACCACTACATTCAGTAGTTTAGATGCCTAGAATAAATA	580 00883
Oy	8581	GGAAGGAGATGGCTCTTCTTGTCTCATTGTGTTTCTTCTGAGTGAG	640
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Qy	8641	GAAGGGAACAGCAGAAACAACCAACTGATCCTCAGCTGTCATGTTTCCTTTAAAAGTC 8'	700
Db	200944		01003
QY	8701	CCTGAAGGAAGGTCCTGGAATGTGACTCCCTTGCTCCTCTGTTGCTCTTTGGCATTCA 8	8760
Db	201004		201063
Qy	8761	TITCITIGGACCCIACGCAAGGACTGIAATIGGIGGGGACAGCTAGIGGCCCTGCTGGGC 8	820

202143 202203 201064 TTTCTTTGGACCCTACGCAAGGACTGTAATTGGTGGGGACAGCTAGTGGCCCTGCTGGGC 201123 201243 201363 201423 201543 201663 201783 201843 201903 201963 202083 201303 9420 9480 9540 0096 0996 9720 9840 8880 8940 0006 0906 9120 9180 9240 9360 0066 TTAAACCATTTTTTTTTTTGTGGTTAGAAAAGTTATGTAGAAAAAAGTAAAATGTGATTT GCTGCATAAATGTGGTACAAGCATTCTGTCTTGAAGGGCAGGTGCTTCAGGATACCATAT GCTGCATAAATGTGGTACAAGCATTCTGTCTTGAAGGCAGGTGCTTCAGGATACCATAT CTCGGCTCACTGTAACCTCTGCCTCCCAGGTTCAAGCGATTCTCCTGTCTCCAGCCTCCCA AGAGTCTTAATATATATATCCAGATGCCATGTGTTTACTTTATGTTACTACATGCACTTG ACGCTCATTGTAGAAAAGCTATAAAATGAATACAATTAAAGCTGTTATTTAATTAGCCAG TGAAAAACTATTAACAACTTGTCTATTACCTGTTAGTATTATTGTTGCATTAAAAATGCA TATACTTTAATAAATGTATATTGTATTGTATACTGCATGATTTTATTGAAGTTCTTGTTC CTTTACATTTTGTCTTACGGAATATTTTCATTCAACTGTGGTAGCCGAATTAATCGTGTT CCTCAATGAAGTGGAGTAAGCTCTCTCATTTTGAGATGGTATAATGGAAGCCACCAAGTG AAAATCTAACCAGGACATTCAGGAATTGCTAGATTCTGGGAAATCAGTTCACCATGTTCA AAAGAGTCTTTTTTTTTTTTTGAGACTCTATTGCCCCAGGCTGGAGTGCCATGAT CTCGGCTCACTGTAACCTCTGCCTCCCAGGTTCAAGCGATTCTCCTGTCTCAGCCTCCCA AGTAGCTGGGATTACAGGCGTGCACCACCATGCCCGGCTAATTTTTGTATTTTAGTAGA TGCCTCGGCCTCCCAAAGTGCTGAGATTACAGGTGTGAGCCACCCTGCCCAGCCGTCAAA ACAGCTCAGAAGTTTCTTCTTTAGGCATTAAAATTTTAGCAAAGATATCTCATCTTCTT TTAAACCATTTTTTTTTTTTGGGTTAGAAAGTTATGTAGAAAAAAGTAAATGTGATTTT GCTTAGAGGATGCCCAGGTCCTTCCATGGAGCCACTGGGGTTCCGGTGCACATTAAAAAA 9541 1906 9361 9421 9481 9661 9721 8821 8941 9121 9181 9241 9301 9601 9781 202084 9841 Db 202144 201184 201244 9001 201424 201484 201544 201604 201724 201784 201844 201904 201964 202024 201124 8881 201304 201364 201664 q g qq οp g δy δŏ 셤 δλ 염 q QQ qq δλ g δŏ Db δŏ ŏ δ ò g Qγ Qγ δy δλ g οy g qq qq δ δy $\delta \lambda$ δy

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5816 5936 5996 5456 5516 5576 5636 9699 5756 5876 6824 5216 5336 5396 6344 6404 6464 6524 6644 6704 6884 5096 5984 6044 6104 5276 6164 6224 6284 6584 6057 ACCCTAGTCATTGGAGTCATCAGTGGAATTGCTGTTTTTGTCGTCATCTTGTTCATTGGA 6116 6645 ATTGCCCAATGGGGGTGGGACCTACCAGGCTGGATAACCTTGGCTGTACCCCCTGGGGA 6465 TCTCCTCATCCTTCCTCTTTCCTGTCAAGTGCCTCCTTTGGTGAAGGTGAAGTACATCATGT AGAGCAGAGATATACGINCCAGGIGGAGCACCCAGGCCTGGATCAGCCCCTCATIGIGAT CTGGGGTATGTGACTGATGAGAGCCAGGAGCTGAGAAAATCTATTGGGGGGTTGAGAGGAG GAGGGTGGCAATCAAAGGCTTTAACTTGTTTTCTGTTTTAGAGCCCTCACCGTCTGGC CTGAGCCAAGATCGCGCCACTGCACTCCAGCCTAGGCAGCAGAGTGAGACTCCATCTTAA **AAAAAAAAAAAAAAAAAAAAAAAAATTCAGAGATCTCAGCTATCATATGAATACCAGGA** ATGCCTCCTAGGTTGACCCAGGTGAAACTGACCATCTGTATTCAATCATTTTCAATGCAC 6285 TGTGAGGAGAACAAGCTGATCTGACTCTCCAAGTGACACTGTGTTAGAGTCAATCT TAGGACACAAAATGGTGTCTCTCTGTAGCTTGTTTTTTTCTGAAAAGGGTATTTCCTTC TAGGACACAAAAATGGTGTCTCCCTGTAGCTTGTTTTTTTCTGAAAAGGGTATTTCCTTC CTCCAACCTATAGAAGGAAGTGAAAGTTCCAGTCTTCCTGGCAAGGGTAAAACAGTCCCC CTCCAACCTATAGAAGGAAGTGAAAGTTCCAGTCTTCCTGGCAAGGGTAAACAGATCCCC TCTCCTCATCCTTCCTCTTTCCTGTCAAGTGCCTCCTTTGGTGAAGGTGACACATCATGT GACCTCTTCAGTGACCACTCTACGGTGTCGGGCCTTGAACTACTACCCCCCAGAACATCAC ATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCCCCGGGGGA TGCCTGAGGAGGTAATTATGGCAGTGAGATGAGGATCTGCTCTTTGTTAGGGGGGTGGGCT TCATAGAACATAGCAATAATCACTGAAGCTACCTATCTTACAAGTCCGCTTCTTATAACA TGTGAGGAGAACAAGCTGATCTGACTGCTCTCCAAGTGACACTGTGTTAGAGTCCAATCT 6765 6705 6825 6345 6405 6585 5817 5877 4977 5867 5037 5927 5097 5985 5217 6105 5277 6165 5397 5457 5517 5577 5637 6525 5697 5757 5937 g g qq 9. Pb ØΥ g QY Db QΥ Dp ΟŊ Dp Qγ qq δy QQ Ω qq δy QQ δy g δ g ρy g QΥ q QΥ d ò g δý Ω δ Ω

7004	6176 7064	6236 7124	6296 7184	6356 7244	5416 7304	6476 7364	6536 7424	6596 7484	6656 7544	6716 7604	6776 7664	6836	6896	6956	7016	7076 7964	7136	7196
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6945	6117 7005	6177 7065	6237	6297 7185	6357	6417 7305	6477	6537 7425	6597 7485	6657 7545	6717 7605	6777 7665	6837 7725	6897 7785	6957	7017	7077	7137
QQ	Qy Db	Qy Db	O Dp	Oy Db	S G	oy oy	Qy Dp	Qy	Q Dp	Qy	Qy Pp	Oy Dp	6 G	Oy Dp	Oy Dp	Qy Dp	Qy Dp	, yo

8156 8216 8276 9164 7856 7916 7976 8036 8096 9044 9104 1676 8684 8744 8804 8864 8924 8984 7556 8564 8624 7496 8444 8504 7436 8324 8084 CCATTTCTTTTTAAATGAAGAAGTGAAGTAGGCCGGGCACGGTGGCTCACGCCTGTAA TGGCTAACATGGTGAAACCCCCATCTCTAATAAAAATACAAAAATTAGCTGGGCGTGGTG GAAAATTATGATAAGGATGATAAAAGCACTTACTTCGTGTCCGACTCTTCTGAGCACCTA GAAAATTATGATAAGGATGATAAAAGCACTTACTTCGTGTCCGACTCTTCTGAGCACCTA GTATTCCAGACCTGAAGAATCACAATAATTTTCTACCTGGTCTCTCCTTGTTCTGATAAT 8805 GIAITCCAGACCTGAAGAATCACAATAATTTTCTACCTGGTCTCTCTTGTTCTGATAAT TCCCAGCACTTTGGGAGGCCAAAGCGGGTGGATCACGAGGTCAGGAGATCGAGACCATCC CCATTTAGGTTTCTGAGTTCCTGCATGCCGGTGATCCCTAGCTGTGACCTCTCCCCTGGA AGAGACATACACCTATGTCATTTCATTTTCCTATTTTTGGAAGAGGACTCCTTAAATTTGG GGGACTTACATGATTTTAACATCTGAGAAAAGCTTTGAACCTGGGACGTGGCTAG CITCCATCTGATTGTGATGTGAGTTGCACAGCTATGAAGGCTGTACACTGCACGAATGGA AATTGCCTGACGAACTCCTTGATTTTAGCCTTCTCTGTTCATTTCCTCAAAAAGATTTCC 8745 8985 8157 9045 8625 7977 8865 8037 8925 8097 8217 9105 7677 8565 7737 7197 8685 7857 7917 8265 7437 8325 8382 7557 8445 7617 8505 8205 7377 8025 7197 8085 8145 7317 7497 7257 Db Dρ g Op δ g Qγ οqα qq Db οy οy Ωp δ οy q Qy δy q οy qq δy Ω δy Ωp ΩŊ qq Ω QQ Qγ Ω Ω οy ò

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237 125	TAGAGACAGGGTTTCACCATGTTGGCCAGGCTGGTCTCGAACTCTCCTGACCTCGTGATCTCTTCTTCTTCTTCTTTTTTTT	9296 10184
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10016 10196 10256 10484 10664 10724 10784 10076 10436 9476 9236 9656 9656 9716 9116 9836 9686 9366 10964 11024 11084 11264 10496 CAAAAGAGTCTTAATATATATATCCAGATGGCATGTGTTTACTTTATGTTACTACATGCA ATTICITIACATTITGICITACGGAATATTITCATTCAACTGTGGTAGCCGAATTAAATCG TGTTTCTTCACTCTAGGGACATTGTCGTCTAAGTTGTAAGACATTGGTTATTTTACCAGC AAACCATTCTGAAAGCATATGACAAATTATTCTCTCTTAATATCTTACTATACTGAAAG TATTAGGTAAGCATTTGTTTTATATTGGTTTTTATTTCACCTGGGCTGAGATTTCAAGAAA TTAATTTTTCTGGCTTTATTCATAAATTCTTAAGGTCAACTACATTTGAAAAATCAAAGA GCAGCGCTGAGGGTTTTCCTGAAGGTAAAGGAATAAAGAATGGGTGGAGGGGCGTGCACT ATATACAGCTCAGAAGTTTCTTTTAGGCATTAAATTTTAGCAAAGATATCTCATCTCT CACCCCAGTCTTCACAGTAACACATTTCACTAACACATTTACTAAACATCAGCAACTGTG CCTGCATITIAAATICTTATICACCTCTGGCAAAACCATICACAAACCAIGGTAGTAAAG 9477 9597 10845 10965 9357 9417 9537 10425 9657 9717 9777 9837 10725 6867 9957 10197 11145 10377 10437 10245 10305 10365 10485 10545 10905 10077 10257 10605 10665 10785 10017 10137 11025 11085 10317 11205 11265 qq Ω q g g g qq qq QQ d δý Οy Qy ٥y Ω δy δŽ οy qq δ QY Q q δ δ Ω a δy g ζ a Ω g δ q Qγ

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                            3250: contig of 3250 bp in length
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Homo sapiens chromosome 6 clone RP11-557F22, *** SEQUENCING IN
AL359892
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 193752)
                                                                                                                                                                                                                                           10557 CCAGCTATTTGAATTGCTGGAATCACAGGCCCATTGCTGAGCTGCCTGAACTGGGAACACA 10616
                                                                                                                                                                                                                                                                               10617 ACAGAAGGAAAACAAAACCACTCTGATAATCATTGAGTCAAGTACAGGAGGTGATTGAGGA 10676
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On Aug 27, 2000 this sequence version replaced gi:9864230.
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* This record will be updated with the finished sequence as soon as it is available and the accession number will
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13562 13082 2915 3035 3155 3275 3390 3450 3570 3630 3750 3810 3870 GAGTTTGAGACAAGCTTGGCCAACATGGTGAAACCCCATGTCTACTAAAAATACAAAAAT 3215 ITCAACTACCATGGCTAGACACACCTTAACATTTTCTAGAATCCACCAGCTTTAGTGGAG 3510 3930 | GGGGTAAATCAAGGATCTGCATTTGGGACATGTTAAGTTTGAGATTCCAGTCAGGCTTCC 13680 GGGGTAAATCAAGGATCTGCATTT-GGACATGTTAAGTTTGAGATTCCAGTCAGGCTTCC TGGTCTTTCCTTGTTTGAAGCTTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGA TNATGAGAGTCGCCGTGTGGAGCCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCA CCCTGAAAAAGAGAGAGTTAAAGTTGACTTTGTTCTTTATTTTAATTTTATTGGCCTGA GCAGTGGGGTAATTGGCAATGCCATTTCTGAGATGGTGAAGGCCAGAGGAAAGAGCAGTTT AAGTGGTGAGGCCACATAGGCAGTTCAGTGTAAGAATTCAGGACCAAGGCTGGGCACGGT GGCTCACTTCTGTAATCCCAGCACTTTGGTGGCTGAGGCAGGTAGATCATTTGAGGTCAG AACTGAAGGAATTATTCCTCAGGATTTGGGTCTAATTTGCCCTGAGCACCAACTCCTGAG AGGTGTGTGGAGCCTCAACATCCTGCTCCCCTCCTACTACACATGGTTAAGGCCTGTTGC TCTGTCTCCAGGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCT 2916 13740 2976 3036 3096 3391 3451 3511 3571 13081 3631 3751 3811 3871 2856 3691 13800 3156 13501 3216 13441 3336 13321 13261 13141 13021 12961 12901 12841 원 QQ Q Pp g g QQ g Qy Db QQ g qq QQ qq g Dp Q δλ g δŽ Qγ δ Qγ δý Οy QΥ Ω δ Ωÿ δý Ω ρy QΥ οŻ δ

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QY	13	190
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Dβ	11282	TGGGTAACAGATATGTATTTACATGTGAGGAGAACAAGCTGATCTGACTGCTCTCC
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qq	11162	TTTTTCTGAAAAGGGTATTTCCTTCCTCCAACCTATAGAAGGAAG
Qy	5551	TCCTGGC
qq	11102	CCTGGGAAGGGTAAACAGATCCCCTCTCTTCTTTCCTTTCCTGTCAAGTGCC
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qa	11042	CTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTCGGGC
Qy	5671	5 -
QΩ	10982	GAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGA
QY	5731	GCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGG 5790
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Qy	5791	ATAACCTTGGCTGTACCCCCTGGGGAAGACCAGAGATATACGTNCCAGGTGGAGCACCCA 5850
qa	10862	TAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGCACC
Οy	5851	GGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACGATGAGAGCCAGGAGCTGA 5910
QQ	10802	GCCTGGATCAGCCCCCTCATTGTGTTTTGGGGTATGTGTGTG
Qy	5911	GAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGATGAGG 5970
qq	10742	AAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGGAGATGAGA
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9363 7350 9303 7410 9243 7470 9183 7530 9123 7590 6906 7650 9003 7710 8943 7770 8883 7830 8823 7890 8763 7950 8010 8070 8583 8130 8190 8463 8250 8310 8343 7290 8703 8643 8523 8403 CCGGCCACGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCAAAGCGGGTGC CTGTTCATTTCCTCAAAAAGATTTCCCCCATTTAGGTTTCTGAGTTCCTGCATGCCGGTGA TCCCTAGCTGTGACCTCTCCCCTGGAACTGTCTCTCATGAACCTCAAGCTGCATCTAGAG GCTTCCTTCATTTCCTCCGTCACCTCAGAGACATACACCTATGTCATTTCCTATT TITGGAAGAGGACTCCTTAAATTTGGGGGACTTACATGATTCATTTTAACATCTGAGAAA AGCTTTGAACCCTGGGACGTGGCTAGTCATAACCTTACCAGATTTTTACACATGTATCTA TGAAGGCTGTACACTGCACGAATGGAAGAGGCACCTGTCCCAGAAAAAGCATCATGGCTA TCTGTGGGTAGTATGATGGGTGTTTTTAGCAGGTAGGAGCCAAATATCTTGAAAGGGGTT GTGCCTTCATTTGGGATGCTACTCTAGTATTCCAGACCTGAAGAATCACAATAATTTTCT ACCTGGTCTCTCCTTGTTCTGATAATGAAAATTATGATAAGGATGATAAAAGCACTTACT **ATTCTATGAGATAGGTACTATTATCCCCATTTCTTTTTAAATGAAGAAAGTGAAGTAGG** CCGGGCACGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCCAAAGCGGGTGGATC ACGAGGTCAGGAGATCGAGACCATCCTGGCTAACATGGTGAAAACCCCCATCTCTAATAAAA 9002 8942 8762 8191 8402 9422 9362 7351 9302 7411 9242 7471 9182 7531 9122 7591 9062 7651 7711 7771 8882 7831 8822 8702 8642 8071 8582 8522 8462 8251 7231 7291 7891 7951 8011 8131 Q qq qq οg QQ g QQ οy δ δý QΥ δ οy δ δ QQ δ Q οy g δ g δ q οy g οy qq òγ g ò g δ QQ ŏ a

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70 42	9151	21
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οy	39	TGTTTACTTTATGTTACTACATGCACTTGGCTGCATAAATGTGGTACAAGCATTCTGTC 945
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Direct Submission
L. Submitted (26-FBB-1997) Sequencing, Mercator Genetics, 4040
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Location/Qualifiers
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1 (bases I to 24682)
Ruddy,D.A., Kronmal,G.S., Lee,V.K., Mintier,G.A., Quintana,L., Domingo,R. Jr., Moyer,N.C., Irrinki,A., McClelland,E.E., Fullan,A., Mapa,F.A., Moore,T., Thomas,W., Loeb,D.B., Harmon,C., Tsuchinashi,Z., Wolff,R.K., Schatzman,R.C. and Feder,J.N. A 1.1-Mb transcript map of the hereditary hemochromatosis locus Genome Res. 7 (5), 441-456 (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds. U91328
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90 Q	6	Qy Db	oy Dp	Oy Dp	Qy Db	Qy Db	Qy Db	Qy Db	oy Dp	Oy Dp	S S	Qy Db	Oy Dp	දු පු	Oy Dp	6 6 6	ôy Ob

51399 51339 51159 50920 51279 2760 2880 2940 2580 2640 2700 2820 2280 2340 2400 2460 2520 GCTGGGTGTGGTGGCATGCACCTGTGATCCTAGCTACTCGGGAGGTGAGGTGAAGGTA TTCTGAGATGGTGAAGGCAGAGAGAAGAGCAGTTTGGGGTAAATCAAGGATCTGCATTTG CAGTGFAAGAATTCAGGACCAAGGCTGGGCACGGTGGCTCACTTCTGFAATCCCAGCACT TATATICTGAAGGAAGTTGCTGAAGGATTCTATGTTGTGTGAGAGAAGAAGAATTGG GTTCAAGACCAGCCTGGGCAACACACAGCAAAAACCCCTTCTTCTCTACAAAAATACAAAAATTA TGACTTTGTTCTTTATTTAATTTTAATTGGCCTGAGCAGTGGGGTAATTGGCAATGCCAT GGACATGTTAAGTTTGAGATTCCAGTCAGGCTTCCAAGTGGTGAGGCCACATAGGCAGTT CTGGGTGTAGTAGCTCATGCCAAGGAGGAGGCCAAGGAGAGCAGATTCCTGAGCTCAGGA GCTGGGTGTGGTGCATGCACCTGTGATCCTAGCTACTCGGGAGGCTGAGGTGGAGGTA CTAGGTGACAGAGCAAGACCCTGTCTCCCCTGACCCCCTGAAAAAGAGAAGAGTTAAAGT AAGGGAGCAACAGTAAAAGCAGGGAGCCCAGCAGGAAGCTGTTACACAGTCCAGGCAAG AGGTAGTGGAGTGGGCTGGGTGGGAACAGAAAAGGGAGTGACAAACCATTGTCTCCTGAA CGGCGTGGGGGAAGGGGGACTACCATCTGCATGTAGGATGTCTAGCAGTATCCTGT CCICCCIACICACIAGGIGCIAGGAGCACICCCCCAGICITGACAACCAAAAAIGICICI AATAAACAAGTAGTGCTGGGGGAGTAGAGGCCAAGAAGTAGGTAATGGGCTCAGAAGAGGA GCCACAAACAAGGTTGTGCAGGCGCCTGTAGGCTGTGGTGTGAATTCTAGCCAAGGAGTA 51038 3061 51938 2101 2161 2221 2281 2341 2401 2461 2521 2581 2641 51278 2761 51218 51158 2881 2941 3001 50979 50919 2701 51098 2041 51878 51818 51758 51698 51638 51578 51518 51458 51398 51338 2821 QQ Dp QΩ qq g qq òγ Dp ò g QΥ QQ δý Ωp Qγ g Ωý qq οy d ò g Q Вþ g QQ Qγ οy δy οy δy δλ Óγ Óλ δý οy

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Oy Dp	3421 50559	TCTAATTTGCCCTGAGCACCAACTCCTGAGTTCAACTACCATGGCTAGACACACCTTAAC 3480 	
OY Db	3481	ATTTCTAGAATCCACCAGCTTTAGTGGAGTCTGTCTAATCATGAGTATTGGAATAGGAT 3540 	
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οy	4201	CACACCTGCAGGTCATCCTG 426	

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49779	4261	4321	4381 49599	4441	4501	4561 49419	4621 49359	4681 49299	4741	4801 49179	4861	4921 49059	4981	5041 48939	5101 48879	5161 48819	5221 48759	5281
qa	A da	Qy	Qy	QY	Qy Db	QY Db	QY	Qy Db	Qy Db	Qy Db	Qy Db	Qy Db	Qy Db	Qy Db	Qy	QY	Qy	δy

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CTAGGTTGACCCAGGTGAAACTGACCATCTGTATT	AGGGCAATTTTATCTATCAGAACAAAGAACATGGGTAACAGATATGTATATTTACATGT 	AGGAGAACAAGCTGATCTGACTGCTCTCCAAGTGACACTGTGTTAGAGTCCAATCTTAGG 	ACACAAAATGGTGTCTCTCTGTAGCTTGTTTTTTCTGAAAAGGGTATTTCTTCTCC 	aacctatagaaggaagtgaaagttccagtcttcctggcaagggtaaacagatccctv 	TCCTTCCTCTTTCCTGTCAAGTGCCTCCTTTGGTGAAGGTGACACATCATGTGAC 	CTTCAGTGACCACTCTACGGTGTCGGGCCTTGAACTACTCCCCCAGAACATCACCAT 	aagtggctgaaggataagcagccaatggatgccaaggagttcgaacctaaagacgtatt 	CCCAATGGGGATGGGACCTACCAGGCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAG 	CAGAGATATACGTNCCAGGTGGAGCACCCAGGCCTGGATCAGCCCCTCATTGTGATCTG 	igtgactgatgagagccaggagctgagaaatctattgggggttgagaggagtgc 	GAGGAGGTAATTATGGCAGTGAGATCTGCTCTTTGTTAGGGGGTGGGCTGAGG 	GTGGCAATCAAAGGCTTTAACTTGCTTTTTCTGTTTTAGAGCCCTCACCGTCTGGCAACCC 	TAGTCATTGGAGTCATCAGTGGAATTGCTGTTTTTGTCGTCATCTTGTTCATTGGAATTT 	GTTCATAATATTAAGGAAGAGGCAGGGTTCAAGTGAGTAGGAACAACAAGGGGGAAGTCTCT 	TAGTACCTCTGCCCCAGGGCACAGTGGGAAGAGGGGCAGAGGGGATCTGGCATCCATGG 	aagcattititctcatttatattctttggggacaccagcagctccctgggagacagaaat 	AATGGTTCTCCCCAGAATGAAAGTCTCTAATTCAACAACATCTTCAGAGCACCTACTAT 	TTTGCAAGAGCTGTTTAAGGTAGTAGAGGGCTTTGAGGTTGAGATGAGAGTCACTGTGGCTAT
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47020 46660 47200 46960 46900 46480 6840 7080 7140 7260 7320 7380 7440 0999 6720 6780 6900 0969 7020 7200 TTAGETTTCTGAGTTCCTGCATGCCGGTGATCCCTAGCTGTGACCTCTCCCCTGGAACTG CTTTCCTGGGTCTCTTGTCTCCACAGGAGGAGCCATGGGGGCACTACGTCTTAGCTGAACG TGAGTGACACGCAGCCTGCAGACTCACTGTGGGAAGGAGACAAAAACTAGAGACTCAAAGA TCACTGGGGTGTCATTGAAGGATCCTAAGAAAGGAGGACCACGATCTCCCTTATATGGTG AATGTGTTGTTAAGAAGTTAGATGAGAGGTGAGGAGACCAGTTAGAAAGCCAATAAGCAT GGGAGTGCATTTATGAGCTCTTCATGTTTCAGGAGAGAGTTGAACCTAAACATATT **ACATACACCTATGTCATTTCCTATTTTTGGAAGAGGACTCCTTAAATTTGGGGGA** ACCCCATGAGGTCCTAAAGCAGGAGGAAGCAAATGCTTAGGGTGTCAAAGGAAAGAATG ATCACATTCAGCTGGGGATCAAGATAGCCTTCTGGATCTTGAAGGAGAAGCTGGATTCCA AGCTATCACTCACCAATTATGCATTTCTACCCCCTGAACATCTGTGGGGTGTAGGGAAAAGA GAATCAGAAAGAAGCCAGCTCATACAGAGTCCAAGGGTCTTTTGGGATATTGGGTTATGA 6781 6841 47139 6901 6961 7021 46899 7141 7201 46779 7261 7321 7381 7441 6541 6601 6661 6721 7081 6421 47559 6481 47379 47319 47259 47199 47079 47019 46959 46839 46719 46659 46539 47499 47439 Dp QQ Ωp Dp qq qq Dp qq Db g Dp g g qq g g QQ QQ δý δy QY δy οy òγ δ Qγ Qγ óγ Ω ò οy οy Ω δy Óγ Qγ

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Direct submission

Submitted (05-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: hunquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Jun 26, 2000 this sequence version replaced gi:865345.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone amme. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EMBL: Sw.; SWISSPROT; Tr:, TREMBL: Wp:, WORNPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping http://www.sanger.ac.uk/RIGP/Chic and at found at http://www.sanger.ac.uk/RIGP/Chic and at found at http://www.sanger.ac.uk/RIGP/Chic and at found at http://www.sanger.ac.uk/RIGP/Chic and a found at a found at http://www.sanger.ac.uk/RIGP/Chic and a found at http://www.sanger.a
                                                                                                                                                                                                                                                           AL353759 101099 bp DNA linear PRI 05-SEP-2001 Human DNA sequence from clone RPI-221C16 on chromosome 6. Contains the 3' part of the HFE gene for haemochromatosis protein, two genes for novel histone 4 family members, two genes for novel histone 1 family members, the genes for novel histone 1 genes for novel histone 2 family member, a novel pseudogene, AL353759
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HTG; CpG island; H1; H2A; H2B; H4; haemochromatosis; HFE; histone.
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Mammalla, Eutherla, Primates; Catarrhini, Hominidae, Homo,
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10801 TAAAATCCCCAAATTTTTCATAAAC 10825
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/clone_lib="RPCI-1"
204. .414
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         misc_feature
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/note="Single clone region. Sequence confirmed by U91328
and assembly confirmed by restriction digest."
4717. .4799
/note="LIMA4A repeat: matches 6189. .6275 of consensus"
4816. .4979
match: ESTs: Em:N93736 Em:R07696 Em:R47761 Em:A1763178
Em:R07647 Em:R50396 Em:A1127651 Em:A8450694 Em:AA319758
Em:R1949947 Em:A1122894 Em:A1040303 Em:AW469921"
/product="dJ221C16.10.1 (hemochromatosis protein)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1127. .1305
/note="MER91B repeat: matches 12. .174 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              consensus
                                                                                                                                                                                                                       /note="isoform 2, splice variant delE2(14E4)
match: CDNAs: Em:AF079407 Em:AF079409 Em:AF079408"
/product="dJ221C16.10.2 (haemochromatosis protein)"
/evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3154. .8275 
/note="FLAM_C repeat: matches 9. .127 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1427. 1554

/note="MIR repeat: matches 121. 241 of consensus"

/note="MIR repeat: matches 1. 308 of consensus"

/note="Alux repeat: matches 1. 308 of consensus"

1863. 1944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(2103. .2404)
/note="match: STS: Em:G22425"
/495. .2780
//note=#alusg repeat: matches 1. .294 of consensus"
3135. .3140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5232. .5532

/note="AluSx repeat: matches 1. .298 of consensus"

5547. .5825

/note="AluJo repeat: matches 1. .295 of consensus"

6160. .6457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /evidence=not_experimental
/protein_di221c16.10.1 (hemochromatosis protein)"
/protein_d="CAC14161.1"
/db_xref="G1:10944580"
/db_xref="SPTREMBL:09H4X3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .299 of consensus'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / 195. .7322 -- reat: matches 1. .311 of cc // note="AluJb repeat: matches 131. .260 of v 8012. .8059 // note="2 copies 2" -- reat: matches 131. .260 of v // note="2 copies 2" -- reat: matches 131. .260 of v // note="2 copies 2" -- reat: matches 131. .260 of v // note="2 copies 2" -- reat: matches 131. .260 of v // note="2 copies 2" -- reat: matches 131. .260 of v // note="2 copies 2" -- reat: matches 131. .260 of v // note="2 copies 2" -- reat: matches 131. .260 of v // note="2 copies 2" -- reat: matches 131. .260 of v // note="2 copies 2" -- reat: matches 131. .260 of v // note="2 copies 2" -- reat: matches 131. .260 of v // note="2 copies 2" -- reat: matches 131. .260 of v // note="2 copies 2" -- reat: matches 131. .260 of v // note="2 copies 2" -- reat: matches 131. .260 of v // note="2 copies 2" -- reat: matches 131. .260 of v // note="2 copies 2" -- reat: matches 131. .260 of v // note="2 copies 2" -- reat: matches 2" -- reat:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .121 of
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/note="2 copies 24 mer 100% conserved"
8529. .9065
/note="match: GSS: Em:AQ768314"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ....ce="2 copies 24 mer 95% conserved" 8017. .8062 //note="23 copies 7
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/note="AluJb repeat: matches 1.6888. .7194
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complement(6443. .6725)
/note="match: GSS: Em:AQ092256"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       match: proteins: Sw:Q30201"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="GAMGHYVLAERE"
                                                                                                                                  /evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note="isoform 1
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3155. 317
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3176
                                                                                                                                                                                                                                                                                                                                                                          /gene="HFE"
<533. .573
                                                                                                                                                                                                                                                                                                                                                                                                              <533. .573
/gene="HFE"
                                                                                                                                                            <533. .577
/gene="HFE"
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                                                                                                                                                            mRNA
                                                                                                                                                                                                                                                                                                                                                          gene
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/product="dJ221c16.1 (novel histone 4 family member)"
/protein_id="CACO4128.1"
/protein_id="CACO4128.1"
/d_xref="G1:98636G4"
/translation="MSGRGGGGGGGGGGGGRKHRKVLRDNIQGITKPAIRRIARRGGV
KRISGLIYEETRGVLKVFLENVIRDAVTYTEHAKRKTVTAMDVVYALKRGGFTLYGFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MLFAGYYILRFSVVMSETVPAASASAGLAAMEKLPTKKRGRKPA
GLISAGKWPPNLSVSKLITEALSVSQBRGMGSLVALKKALLAAGYDVBRNNSRTKLSL
GSLNNKGIIVQTRGGAGSFRLSKKVIPKGTRSKARKSVSAKTKIVLSKSKSPK

KSLVNKGIIVQTRGGAGGSFRLSKKVIPKGTRSKAKKSVSAKTKIVLSKSKSFRYA
AKTINKRAKKPRATTPKTVRSGRKAKGAKGKOKOKSPVKARASKSKLTQHHEVNVRKAT
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                                                                                 Em: AA868008 Em: AI589002 Em: AA579847
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6575 GATCTTGAAGGAGAAGCTGGATTCCATTAGGTGAGGTTGAAGATGATGGGGGGGTCTACAC 6634
                                                                              /note="match: ESTS: Em:AA868008 Em:AI589002 Em:AA57984
Em:AA25502 Em:AW274802 Em:AR030357 Em:AW55281
Em:AA25502 Em:AW274805 Em:AW374805 Em:AA7474172
Em:AA773487 Em:AA255529 Em:AW005063 Em:AA27555
Em:AA773487 Em:AA25695 Em:AW005063 Em:AA27555
Em:AA70301c1 = AGJ221116.1 (novel histone 4 family member)"
/evidence=not_experimental
10279. 10656
10294. 10665
                                                                                                                                                                                                                                                                                                                                                                                                /note="match: proteins: Tr:P91878 Sw:P02304 Sw:P02306
Sw:P02307 Sw:P02308 Sw:P50566 Sw:Q27443 Sw:P04915
Sw:P35057 Sw:P35059 Sw:P27996"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /evidence=not_experimental
/product="dJ221C16.2 (novel histone 1 family member)"
/protein_id="CAC04129.1"
/db_xref="GG1:9863665"
/db_xref="SPTREMBL:Q9H4X2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note=_nanb lepeat: matches 1. .337 of consensus 13591. .1367 / note="Aludo repeat: matches 44. .114 of consensus" complement(13811. .14476) / gene="da221016.2" complement(13811. .14476) / gene="da221016.2" / fone="da221016.2" / note="match: proteins: Sw:P06893 Sw:P43274 Sw:P40286 Sw:P43275 Sw:P06348 Sw:P06349 Sw:P43277 Sw:P10412 Tr:QQQVBS Sw:P06348 Sw:P06349 Sw:P13865 Tr:Q31369 Sw:P16402 Sw:P16804" Sw:P15864 "
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13241. .13590
//note="MERIB repeat: matches 1. .337 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="AluSg1 repeat: matches 3. .300 of consensus"
13069. .13240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44. .114 of consensus"
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/note="AluJo repeat: matches 1. .261 of consensus"
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Em: AQ751497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
/evidence=not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="dJ221C16.1"
10656
GSS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="dJ221C16.1"
10871. .11142
                                                   /gene="dJ221C16.1"
                                                                                                                                                                                                                                                                                                                                                                     /gene="dJ221C16.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
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qq	61	AGACGGAGCAACCATGCCAAGTAGGAGAGTATAAGGCATACTGGGAGATTAGAAATAATT 120	
6 67 6	121	ACTGTACCTTAACCCTGAGTTTGCGTAGCTATCACCAATTATGCATTTCTACCCC 6754	
Qy Db	6755 181	TGAACATCTGTGGTGTAGGGAAAAGAGAATCAGAAAGAGCCAGCTCATACAGAGTCCAA 6814 	
Qy Dp	6815 241	GGGTCTTTTGGGATATTGGGTTATGATCACTGGGGTGTCATTGAAGGATCCTAAGAAAGG 6874 	
Oy Dp	6875 301	AGGACCACGATCTCCCTTATATGGTGAATGTGTTAAGAAGTTAGATGAGAGGTGAGG 6934 	
9 0 0	6935 361	AGACCAGTTAGAAAGCCAATAAGCATTTCCAGATGAGAGATAATGGTTCTTGAAATCCAA 6994 	
oy Op	6995	TAGTGCCCAGGTCTAAATTGAGATGGGTGAATGAGGAAAATAAGGAAGAGAGAGAGGCA 7054 	
Oy Dp	7055	AGATGGTGCCTAGGTTTGTGATGCCTCTTTCCTGGGTCTCTTGTCTCCACAGGAGCC 7114	
Oy Dp	7115	ATGGGCACTACGTCTTAGCTGAACGTGACACGCAGCCTGCAGACTCACTGTGGGA 7174	
Qy Dp	7175	AGGAGACAAAACTAGAGACTCAAAGAGGGGGTGCATTTATGAGCTCTTCATGTTTCAGGA 7234 	
Sy do	7235	GAGAGTIGAACCTAAACATAGAAATTGCCTGACGAACTCCTTGATTTTAGCCTTCTCTGT 7294 	
oy B	7295	TCATTTCCTCAAAAAGATTTCCCCATTTAGGTTTCTGAGTTCCTGCATGCCGGTGATCCC 7354 	
O.Y Db	7355	TAGCTGTGACCTCTCCCCTGGAACTGTCTCTCATGAACCTCCAAGCTGCATCTAGAGGCTT 7414	
Oy Dp	7415	CCTTCATTTCTCCGTCACCTCAGAGACATACACCTATGTCATTTCATTTCTATTTTG 7474	
9 Pp	7475	GAAGAGGACTCCTTAAATTTGGGGACTTACATGATTCATTTTAACATCTGAGAAAAGCT 7534 	
Qy Dp	7535 961	TTGAACCCTGGGACGTGGCTAGTCATAACCTTACCAGATTTTTACACATGTATCTATGCA 7594 	
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٠, ۲۵ وه	715	GCCTGTACACTGCACGAATGGAAGGGCACCTGTCCCAGAAAAAGCATCATGGCTATCTG 7774 	

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   New hereditary hemochromatosis gene products or polypeptides, useful for treating hereditary hemochromatosis in a patient, and as a metal chelation agent alleviating iron overload -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAGGGGCGCTTGCTGCGTGAGTCCGAGGGCTGCGGGCGAACTAGGGGCGCGCGGGGGGTG
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                                          Disclosure; Fig 3; 108pp; English
                                                             invention relates
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Best Local Similarity 100.0
Matches 10823; Conservative
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QY	3001	GACATGTTAAGTTTGAGATTCCAGTTTCCAAGTGGTGAGGGCCACATAGGCAG	3060
đ	3001	atgt	3060
ΟY	3061	AGIGTAAGAATTCAGGACCAAGGCTGGGCACGGTGGCTCACTTCTGTAATCCCAGCAC	3120
ΩD	3061	gtgtaagaattcaggaccaaggctgggca	3120
Qy	3121	TIGGIGGCIGAGGCAGGIAGAICAITICAGGICAGGAGITIGAGACAAGCITGGCCAACA	3180
Qy	3181	GGTGAAAACCCCCATGTCTACTAAAATACAAAATTAGCCTGGTGTGGTGGCGCACGCCCC	24
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Qy	3241	GTTTTCAGGAGGCTTAGGTAGGAGAATCCCTTGAACCCCAGGAGGTGCAG	0
qq	3241	tagtcccaggttttcaggaggc	3300
QY	3301	GGTGATAGAGTGAGACTCT	3360
QQ	3301	tgcagtgagctgagattgtgccactgcactccagcctgggtgatagagtgagactctt	3360
Οy	3361	TGAAGGAATTATTCCTCAGGATTTGG	3420
qq	3361	IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	3420
Qy	3421	AGTTCAACTACCATGGCTAGACACACCTTAA	3480
qq	3421	ctaatttgccctgagcaccaactcctgagtt	8
QY	3481	AATCCACCAGCTTTAGTGGAGTCTGTCTAATCATGAGTATTGGAATAG	3540
QO	3481	ttttctagaatccac	
QÝ	3541	GGGGCAGTGAGGGGGGGGGCACCACGTGTGGCAGAAAAAGCACACAAGGAAAGAGC	3600
qq	3541	tgggggcagtgaggggggggggcagccacgtgtgcagagaaaagcacacaaggaaaagac	3600
Qy	3601	ACTGTCATATGGAAGAAGACAGGACTGCAACTCACCCTTCACAAAATGAGGA	3660
QQ	3601	cccaggactgtcatatggaagaaagacaggactgcaactcacccttcacaaatgaga	
Qy	3661	STATGAGTTGATGCAGGTGTGGAGCCTCAACATCCTGCTCCC	
qa	3661	cagacacagctgattgttttttttttttttttttttttt	
Qγ	3721	GTTAAGGCCTGTTGCTCTGTCTCCAGGTTCACACTCTCTGCACTA	3780
qa	3721	toctactacacatggttaaggcctgttgctctgtctccaggttcacactctctgcacta	
δÿ	3781	SCCTCAGAGGACGACGTCTTTCCTTGTTTGAAGCTTTGGGCTA	3840
qq	3781	ctttcatgggtgcctcagagcaggaccttggtcttccttgtttgaagctttgggcta	3840
QY	3841	TGGATGACCAGCTGTTCGTGTTCTATGATNATGAGAGTCGCCGTGTGGGGCCCCGAAC	3900
qq	3841	gtggatgaccagctgttcgtgttctatgatcatgagagtcgccgtgtggagcccgaac	3900
Qγ	3901	CCATGGCTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGCAGCTGAGTCAGAGTCTGAA	3960
QQ	3901	catgggtttccagtagaatttcaagccagatgtggctgcagctgagtcagagtctgaa :	6
QY	3961	SGIGGGATCACATGTTCACTGTTGACTTCTGGACTATTATGGAAAATCACAACCACAG	4020
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ITGAAGGAAACAGCTGGAAGTCTGAGGTCTTGTGGGAGCAGGGAAGAGGGAAG 4140 	SCTTCCTGAGATCATTGGTCCTTGGGGATGGTGGAAATAGGGACCTATTCCTT 4200 	CAGTTAACAAGGCTGGGGATTTTTCCAGAGTCCCACCCTGCAGGTCATCCTG 4260 	SAAATGCAAGAAGAACAGTACCGAGGCTACTGGAAGTACGGGTATGATGGG 4320 	CACCTTGAATTCTGCCCTGACACTGGATTGGAGAGCAGCAGCAACCCAGGGCC 4380 	ACCAAGCTGGAGTGGGAAAGGCACAAGATTCGGGCCAGGCAGAACAGGGCCTAC 4440 	GGGACTGCCTGCACAGCT 	CAA	GCACGGAA gcacggaa	III Ltc	AGCCACAAGTCATGGGTTTAATTTCTTTTCTCCATGCATATGGCTCAAAGGGAA 4740 	ATGGCCCTTGCTTTTTATTTAACCAATAATCTTTTGTATATTTTATACCTGTTAA 4800 	AGAAATGTCAAGGCCGGGCACGGTGGCTCACCCCTGTAATCCCAGCACTTTGGG 4860 	AGGCGGGTGGTCACAAGGTCTAGAGACTAGCCAGCCTGACCAACATGGTGAA 4920 	CTCTAAAAA ctctaaaaa	TGGAAGGCTGAGGCAGGAGCATGGCTTGAACCTGGGAAGCGGAAGTTGCACTGA 5040 	APTGGGGCCACTGCACCTAGGCAGCAGAGTGAGACTCCATCATAAAAA 5100 	AAAAAAAAAAAAATTCAGAGATCTCAGCTATCATGAATGA
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6120 6180 6240 5700 5820 5940 5940 0009 0009 0909 0909 6120 6180 6300 5520 5520 5580 5580 5640 5640 5700 5760 5760 5820 5880 5880 5400 5400 5460 5460 5280 AAGCATTTTTCTCATTTATATTCTTTGGGGACACCAGCAGCTCCCTGGGAGACAGAAAAT TAGTACCTCTGCCCCAGGGCACAGTGGGAAAGAGGGGCAAGAGGGGATCTGGCATCCATGGG GTGGCAATCAAAGGCTTTAACTTGCTTTTTTTTTAGAGCCCTCACCGTCTGGCACCC AGGAGAACAAGCTGATCTGACTGCTCTCCAAGTGACACTGTGTTAGAGTCCAATCTTAGG aggagaacaagctgatctgactgctctccaagtgacactgtgttagagtccaatcttagg TCTTCAGTGACCACTCTACGGTGTCGGGCCTTGAACTACTACCCCCCAGAACATCACCATG AAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCTAAAAGACGTATTG aggtggctgaaggataagcagccaatggatgccaaggagttcgaacctaaagacgtattg GGTATGTGACTGATGAGAGCCAGGAGCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCC TGAGGAGGTAATTATGGCAGTGAGATGAGGATCTGCTCTTTGTTAGGGGGTGGGCTGAGG **AGGGCAATTTTATCTATCAGAACAAGAACATGGGTAACAGATATGTATATTTACATGTG** AACCTATAGAAGGAAGTGAAAGTTCCAGTCTTCCTGGCAAGGGTAAACAGATCCCCTCTC AGAACATAGCAATAATCACTGAAGCTACCTATCTTACAAGTCCGCTTCTTATAACAATGC 6061 6181 6241 5881 6061 6121 6121 6181 5581 5641 5641 5701 5761 5761 5821 5821 5881 5941 6001 6001 5401 5461 5521 5581 5701 5341 5341 5521 5161 5221 5221 5281 5281 5401 5461 5161 g g δ QY Db g Oy Op δŻ q δ g QΥ Q g QQ QY Db Qy Db δŽ Q òγ OD Qγ g QY q QΥ g ò Db ολ g οy δ οy

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8341 CAGAGCTTGCAGTGAGCGGAGTTTGCGCCACTGCACTCCAGCCTAGGTGACAGAGTGAGA 7741 gcacctgtcccagaaaaagcatcatggctatctgtgggtagtatgatggtgtttttagc ATTATGATAAGGATGATAAAAGCACTTACTTCGTGTCCGACTCTTCTGAGCACCTACTTA CATGCATTACTGCATGCACTTCTTACAATAATTCTATGAGATAGGTACTATTATCCCCAT TICTITITIAAATGAAGAAAGTGAAGTAGGCCGGGCACGGTGGCTCACGCCTGTAATCCC 8161 agcactttgggaggccaaagcgggtggatcacgaggtcaggagatcgagaccatcctggc TAACATGGTGAAACCCCCATCTCTAATAAAATACAAAAATTAGCTGGGCGTGGTGGTGGCAG ACGCCTGTAGTCCCAGCTACTCGGAAGGCTGAGGCAGGAGAATGGCATGAACCCAGGAGG 8341 cagagottgcagtgagccgagtttgcgccactgcactccagcctaggtgacagagtgaga ttaggtttctgagttcctgcatgccggtgatccctagctgtgacctctcccctggaactg CATCTGATTGTGATGTGGAGTTGCACAGCTATGAAGGCTGTACACTGCACGAATGGAAGAG GCACCTGTCCCAGAAAAGCATCATGGCTATCTGTGGGTAGTATGATGGTGTTTTTAGC AGGTGTCATACAGATTTGCAAAGTTTAATGGTGCCTTCATTTGGGATGCTACTCATAT TCCAGACCTGAAGAATCACAATAATTTTCTACCTGGTCTCTCCTTGTTCTGATAATGAAA AGCACTTTGGGAGGCCAAAGCGGGTGGATCACGAGGTCAGGAGATCGAGACCATCCTGGC ACATACACCTATGTCATTTCATTTCCTATTTTGGAAGAGGACTCCTTAAATTTGGGGGA CTTACATGATTCATTTTAACATCTGAGAAAGCTTTGAACCCTGGGACGTGGCTAGTCAT TTGAATCCTCTCTCTGTGTTACCCAGTAACTCATCTGTCACCAAGCCTTGGGGATTCTTC **AACCTTACCAGATTTTTACACATGTATCTATGCATTTTCTGGACCCGTTCAACTTTTCCT**

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Matches 10823; Conser
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The present invention relates to hereditary hemochromatosis gene products. These proteins may be used to treat a patient diagnosed as having human hemochromatosis disease. It is also useful as a metal chelation agent or as a T-cell differentiation factor, and for alleviating iron overload. They may also be used in protein replacement therapy for individuals having a defective human hemochromatosis gene.
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Matches 10823; Conse
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                                                                                                                                                                         04-APR-1996;
16-APR-1996;
23-MAY-1996;
                                                 Homo sapiens
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	AGCCCGAGCGGGTGGTCACAAGGTCAGGAGTTTGAGAC 	ACCGGCTCTAAAAAAATACAAAAATTAGCTGGTCACAGG 	GCTAATTGGAAGGCTGAGGAGGAGCATCGCTTGAACCTG 	GCCAAGATCGCGCCACTGCACTCCAGCTAGGCAGCAGGAGG 	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	ATATCAAGTGAGGCCACTTATCAGAGTAGAAGAATCCTT 	AGAACATAGCAATAATCACTGAAGCTACCTATCTTACAA(CTCCTAGGTGACCCAGGTGAAACTGACCATCTGTATTC. 	AGGGCAATTTATCTATCAGAACAAAGAACATGGGTAACA 	AGGAGAACAAGCTGATCTGACTGCTCTCCAAGTGACACTCT 	ACACAAAATGGTGTCTCCTGTAGCTTGTTTTTTTCTG 	AACCTATAGAAGGAAGTGAAAGTTCCAGGTCTTCCTGGCAA 	CTCATCCTTCCTCTTCCTGTCAAGTGCCTCCTTTGGTG 	TCTTCAGTGACCACTCTACGGTGTCGGGCCTTGAACTAC 	AAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAG 	CAATGGGGATGGGACCTACCAGGGCTGGATAACCTTG 	CAGAGATATACGTNCCAGGTGGAGCACCCAGGCCTGGAT(SAGCTGAGAA
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AGGTTTGTGATGCCT 7080 aggtttgtgatgcct 7080	CGTCTTAGCTGAACG 7140 	CTAGAGACTCAAAGA 7200 	CTAAACATAGAAATT 7260 	AAAAAGATTTCCCCAT 7320 	TCTCCCTGGAACTG 7380 	TCCGTCACCTCAGAG 7440 tccgtcacctcagag 7440	CTTAAATTTGGGGGA 7500 	GACGTGGCTAGTCAT 7560 	GGTTCAACTTTCCT 7620 	CCTTGGGGATTCTTC 7680 	TGCACGAATGGAAGAG 7740 	SATGGGTGTTTTAGC 7800 	TTCTAATTGGCATGA 7860 Ltctaattggcatga 7860	GATGCTACTCTAGTAT 7920 	TTGTTCTGATAATGAAA 7980 	TCTGAGCACCTACTTA 8040 	GTACTATTATCCCCAT 8100
TGAATGAGGAAAATAAGGAAGAGAGAAGAGGCAAGATGGTGCCT. 	TTTCCTGGGTCTCTTG tttcctgggtctcttg	AGTGACACGCAGCCTGCAGACTCACTGTG 	GGGAGTGCATTATGAGCTCTTCATGTTTCAGGAGAGAGTTGAAC 	3ATTTTAGCCTTCTCTGTTCATTTCTC 	TTAGGTTTCTGAGTTCCTGCATGCCGGTGATCCCTAGCTGTGACC 	CATGAP	rgrcarrrcarrrcc 	TTTAACATCTGAGAAA 	CCTTACCAGATTTTTACACATGTATCTATGCATTTTCTC 	TTGAATCCTCTCTCTGTGTTACCCAGTAACTCATCTGTCACCAAGC(CTGATTGTGATGTGAGTTGCACAGCTATGAAGGCTGTAC 	GTCCCAGAAAAACCATCATGCTAT 	GGTAGGAGGCAAATATCTTGAAA 	GGTGTGTGAGATTTGCAAAGTTTAATGGTGCCTTCA GGTGTCATAAAGATTTGCAAAGTTTAATGGTGCCTTCA 99tgtcatacagatttgcaaagtttaatggtgccttca	VTCACAATAATTTTCTACCTGGTCTCTCC 	ATTAFGATAAGGATGATAAAAGCACTTACTTCGTGTCCGACTCT" 	CATGCATTACTGCATGCACTTCTTACAATAATTCTATGAGATAG
7021 G 7021 g	7081 C	7141	7201 (7261	7321	7381	7441	7501	7561 7561	7621	7681	7741	7801		7921	7981	8041
Oy Db	Oy Dp	Qy Db	Oy Db	Oy Dp	Oy Db	oy ep	& 43	ço qa	Qy Db	Qy	Qy	Qy Dp	Q Dp	Oy Dp	Oy Db	Oy Db	Qy

9240 8880 8940 8940 0006 9000 0906 9060 9120 9120 9180 9180 8640 8700 8760 8820 8820 8880 8520 8520 8580 8580 8700 8760 8400 8400 8460 8460 AGTAGCTGGGATTACAGGCGTGCACCACCATGCCCGGCTAATTTTTGTATTTTAGTAGA CCTGAAGGAAGGTCCTGGAATGTGACTCCCTTGCTCCTGTTGCTCTTTGGCATTCA CCTCAATGAAGTGGAGTAAGCTCTCTCATTTTGAGATGGTATAATGGAAGCCACCAAGTG AAAGAGTCTTTTTTTTTTTTGAGACTCTATTGCCCCAGGCTGGAGTGCAATGGCATGAT CICGGCICACIGIAACCICIGCCICCCAGGIICAAGCGAIICICCIGICICAGCCICCCA TTCACACACGGTGTCCTCCCTAGGCCAGTGCCTCTGGAGTCAGAACTCTGGTGGTATTTC ACGCCTGTAGTCCCCAGCTACTCGGAAGGCTGAGGCAGGAGAATGGCATGAACCCAGGAGG TAGAGTATCTCATAGTTTGTCAGTGATAGAAACAGGTTTCAAACTCAGTCAATCTGACCG GAAGGGGAACAGCAGAAAACAACCAACTGATCCTCAGCTGTCATGTTTCCTTTAAAAGTC AGCACTTTGGGAGGCCAAAGCGGGTGGATCACGAGGTCAGGAGATCGAGACCATCCTGGC 8881 8941 8941 9001 9001 9061 9061 9181 8761 8761 8821 8881 9121 9121 8641 8701 8401 8461 8461 8521 8581 8581 8641 8701 8101 8221 8221 8281 8341 8341 8401 8521 8101 8161 8161 8281 g qq οy qq δ g g δy δŽ Oy Op Dp δλ Dp ΩY οy g Op δ Q QQ οy g οy g Qγ Ω δý q δ Db Qy οχ QΫ́

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										9781	9841	9901	9961	10021	10081	10141	10201

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ttcataaattcttaaggtcaactacatttgaaaaatcaaagacctg 10320
                                                         GGCCATAGGTAAATGTACCACGGTGGTCCGGTGACCAGAGATGCAG 10440
                                                                    CTGAAGGTAAAGGAATAAAGAATGGGTGGAGGGGGCGTGCACTGGAA 10500
                                                                                                          AAAGCCCCTGAAAATTTGAGAAAACAAACAAGAAACTACTTACCAG 10560
                                                                                                                                                Wolff RK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New hereditary hemochromatosis gene products or polypeptides, useful
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for treating hereditary hemochromatosis in a patient, and as a metal chelation agent alleviating iron overload . XX
PS Disclosure; Fig 3; 108pp; English.

XX
CC The present invention relates to hereditary hemochromatosis gene couches. These proteins may be used to treat a patient diagnosed as products. These proteins may be used to treat a patient diagnosed as comparing human hemochromatosis disease. It is also useful as a metal concellation agent or as a T-cell differentiation factor, and for chelation agent or as a T-cell differentiation factor, and for the concellation agent or an expect of the concellation agent of the concellation agent of the concellation and the concellation agent of the concellation age
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ö 099 720 780 840 540 009 900 099 720 780 240 240 360 360 420 420 480 540 Gaps 120 120 180 180 300 300 CAGGGGCGCTTGCTGCGTGAGTCCGAGGCTGCGGGCGAACTAGGGGCCCCGGCGGGGTG 480 9 9 TAAATAAATCTCGTAGTTCCTCACTTGAGCTGAGCTAAGCCTGGGGCTCCTTGAACCTGG AACTCGGGTTTATTTCCAATGTCAGCTGTGCAGTTTTTTCCCCCAGTCATCTCCAAACAGG CCCGGCTCTGCGGAGTGACTTTTGGAACCGCCCACTCCCTTCCCCCAACTAGAATGCTTT ttccccgccccccaaaagaagcggagatttaacggggacgtgcggccagagctggggaa GAAAAATCGAAACTAGCTTTTTCTTTGCGCTTGGGAGTTTGCTAACTTTGGAGGACCTGC **AATATCTAAAGTTCAGATCAGAACATTGCGAAGCTACTTTCCCCAATCAACAACACCCCT** TCAGGATTTAAAAACCAAGGGGGACACTGGATCACCTAGTGTTTCACAAGCAGGTACCTT CTGCTGTAGGAGAGAGAACTAAAGTTCTGAAAGACCTGTTGCTTTTCACCAGGAAGTT TITCCCCGCCCCCCAAAAGAAGCGGAGATTTAACGGGGACGTGCGGCCAGAGCTGGGGGAA ATGGGCCCGCGAGCCAGGCCGGCGCTTCTCCTCTGATGCTTTTGCAGACCGCGGTCCTG **TCTAAGGTTGAGATAAAATTTTAAATGTATGATTGAATTTTGAAAATCATAAATATTTA** Length 10825 ; Indels 22; 2; DB 0; Mismatches Score 10823; Pred. No. 0; Query Match
Best Local Similarity 100.0%;
Matches 10823; Conservative ч 61 121 361 421 481 541 541 601 199 721 721 781 61 181 181 241 241 301 301 361 421 481 601 199 121 g g g ò g g ò g ò g ò ò g Op δ δý ò a ò g ò ò ò 셤 ð a ò

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3120 3120 3240 3300 3300 3360 3420 3420 3480 3360 3480 3540 3540 3720 3600 3600 3660 3720 3780 3780 3840 3840 3900 4020 4080 4080 4081 ATGCATCTTGAAGGAAACAGCTGGAAGTCTGAGGTCTTGTGGGAGCAGGAAGAGGGAAG 4140 GGACATGTTAAGTTTGAGATTCCAGTCAGGCTTCCAAGTGGTGAGGCCACATAGGCAGTT CAGTGTAAGAATTCAGGACCAAGGCTGGGCACGGTGGCTCACTTCTGTAATCCCAGCACT TTGGTGGCTGAGGCAGGTAGATCATTTGAGGTCAGGAGTTTGAGACAAGCTTGGCCAACA TTGCAGTGAGCTGAGATTGTGCCACTGCACTCCAGCCTGGGTGATAGAGTGAGACTCTGT TCTAATTTGCCCTGAGCACCAACTCCTGAGTTCAACTACCATGGCTAGACACACCTTAAC ATAGTCCCAGGTTTTCAGGAGGCTTAGGTAGGAGAATCCCTTGAACCCAGGAGGTGCAGG CTCCTACTACACATGGTTAAGGCCTGTTGCTCTGTCTCCAGGTTCACACTCTGCACTA **ACCCAGGACTGTCATATGGAAGAAGACAGGACTGCAACTCACCTTCACAAAATGAGGA** CGTGGATGACCAGCTGTTCGTGTTCTATGATNATGAGAGTCGCCGTGTGGAGCCCCGAAC TCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGCAGCTGAGTCAGAGTCTGAA CCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCTTGTTTGAAGCTTTGGGCTA 3241 3301 3001 3001 3061 3061 3121 3181 3241 3421 3121 3181 3301 3481 3541 3421 3481 3601 3601 3661 3661 3721 3721 3781 3781 3841 3841 3901 3901 3961 3961 4021 4021 Q οy g δŽ g Qγ QQ δy g δλ QQ Ω qq ÓΫ Q QY Db QΥ g Dp Op g Qγ ò δy Ω ρp QΫ οy QΥ Db ò d ŏ g ŏ

4140	4200	4260 4260	4320	4380	4440	4500	4560 4560	4620	4680	4740	4800	4860	4920	4980	5040	5100	5160	5220
	GAATTIGCTICCTGAGATCATTIGGTCCTTGGGGATGGTGGAAATAGGGACCTATTCCTT	TGGTTGCAGTTAACAAGGCTGGGGATTTTTCCAGAGTCCCACACCTGCAGGTCATCCTG	GGCTGTGAAATGCAAGAAGAACAACAGTACCGAGGGCTACTGGAAGTACGGGTATGATGGG 	AGGACCACCTTGAATTCTGCCCTGACACACTGGATTGGAG 	TGGCCCACCAAGCTGGAGTGGGAAAGGCACAAGATTCGGGCCAGGCAGAACAGGGCCTAC	CIGGAGAGGGACTGCCCIGCACAGCTGCAGTTGCTGGAGCTGGGGAGAGGGTGTTTTG	GACCAACAAGGTATGGTGGAAACACACTTCTGCCCCTATACTCTAGTGGCAGAGTGGAGG	GGTTGCAGGGCAC ggttgcagggcac		TGAGACAGCCACAAGTCATGGGTTTAATTTCTTTTCTCCATGCATATGGCTCAAAGGAA 	GTGTCTATGGCCCTTGCTTTTTATTTAACCAATAATCTTTTGTATA 	AAATTCAGAAATGTCAAGGCCGGGCACGGTGGCTCACCCTTTTTTTT	AGGCCGAGGCGGGTGGTCACAAGGTCAGGA 	ACCGTCTCTAAAAAATACAAAAATTAGCTGGTCACAGTC 	GCTAATTGGAAGGCTGAGGCAGGAGCATGGCTTG 	GCCAAGATCGC 	AAAAAAAAAAAAAAAAAAAAAAAAAAAAATTCAGAGAT 	ATATCAAGTGAGGCCACTTATCAGAGT
4081	4141	4201	4261	4321	4381	4441	4501	4561	4621	4681	4741	4801	4861	4921	4981	5041	5101	5161
QQ	Qy Db	Oy Dp	Oy Dp	ογ Op	Qy Db	Qy Db	oy Db	Oy Db	Qy Db	O.y Db	O. Db	Q Dp	do ob	Qy Dp	Qy Db	Oy Db	Oy Db	ογ ·

Db	5161	atatcaagtgaggccacttatcagagtagaagaatcctttaggttaaaagtttctttc
Οy	5221	~
QQ	5221	gaacatagcaataatcactgaagctacctatcttacaagtccgcttcttataacaatgc 528
Qy	5281	ICCTAGGTTGACCCAGGTGAAACTGACCATCTGTATTCAATCATTTTCAATGCACATAA 534
qa	5281	taggttgacccaggtgaaactgaccatctgtattcaatcatttcaatgcacat
δλ	34	4 4
q	34	gggcaattttatctatcagaacaaagaacatgggtaacagatatgtatatttatctur
Oy.	40	AGGAGAACAAGCTGATCTGACTGTCTCAAGTGACACTGTGTTAAAGTCAATCTTAGG 5460
Dp	40	ggagaacaagctgatctgactgctctccaagtgacactgtgttagagtcaaagtcaaagg 340)
Qy dd	5461	ACACAAAATGGTGTCTCTCTGTAGGTTGTTTTTTTCTGAAAAGGGTATTTCCTTCC
ò	52	CCTATAGAAGGAAGTGAAAGTTCCAGTCTTCCTGGCAAGGGTAAACAGATCCCCTCTC 558
- qa		
ΟŊ	5581	TITICCIGICAAGIGCCICCTITGGIGAAGGIGACACAICAIGIGGG 564
Db	5581	catecttectettecetgteaagtgeeteetttggtgaaggtgaeacateatgtgaee 564
Qy	5641	TCTTCAGTGACCACTCTACGGTGTCGGGCCTTGAACTACCCCCCAGAACATCACCATG 57
qa	5641	tottcagigaccacictacggigicgggccttgaactacccccagaacatcaccatg 570
QY	5701	AAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCTAAAGACGTATTG 576
q	5701	gragoctgaaggataagcagccaatggatgccaaggagttogaacctaaagacgtattg 576
Qy		80 0
ΩP	5761	saatggggatgggacctaccagggctggataaccttggctgtaccccctggggaagag 582
QY	5821	CAGAGATATACGINCCAGGIGGAGCACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGG 58
qa	5821	cagagatatacgtaccaggtggagcacccaggcctggatcagcccctcattgtgatctgg 588
Qγ	5881	GGTATGTGACTGATGAGAGCCAGGAGCTGAGAAATCTATTGGGGGTTGAGAGGAGTGCC 594
qq	5881	atgigacigatgagagccaggagcigagaaaatctatigggggtigagaggagigcc 594
Qy	5941	TGAGGAGGTAATTATGGCAGTGAGATGAGGATCTGCTCTTTGTTAGGGGGTGGGCTGAGG 600
qq	5941	tgaggaggtaattatggcagtgagatgaggatctgctttgttaggggggtgggctgag
Qy	6001	ō
QQ	6001	gocaatcaaaggetttaacttgetttttetgttttagageeeteacegtetggeacec 606
Qy	6061	TAGTCATTGGAGTCATCAGTGGAATTGCTGTTTTTGTCGTCATCTTGTTCATTGGAATTT 612
QQ	6061	tagicatiggagicatcagiggaatigcigittiigicgicatctigitcatiggaati
Οy	6121	TGTTCATAATATTAAGGAAGGAGGGTTCAAGTGAGTGAGT
QD	6121	tgittcataatattaaggaagaggcagggttcaagtgagtaggaacaagggggaagtctc
QY	6181	NGTACCTCTGCCCCAGGGCACAGTGGGAAGAGGGGCAGAGGGGATCTGGCATCCATGGG 624
qq	6181	gtacctctgccccagggcacagtgggaagaggggcagagggggatctggcatccatggg 624
Qy	6241	30
qq	6241	gcatttttctcatttatttttggggacaccagcagctccttgggagacagaaaa

6360	6420 6420	6480 6480	6540 6540	0099	0999	6720 6720	6780	684 0 684 0	0069	0969	7020	7080	7140	7200	7260	7320	7380
AATGGTICTCCCCAGAATGAAAGTCTCTAATTCAACAACATCTTCAGAGCACCTACTAT	TTTGCAAGAGCTGTTTAAGGTAGTACAGGGGCTTTGAGGTTGAGAAGTCACTGTGGCTAT 	TCTCAGAACCCAAATCTGGTAGGGAATGAAATTGATAGCAAGTAAATGTAGTTAAAGAAG 	ACCCCATGAGGTCCTAAAGCAGGAAGGAAATGCTTAGGGTGTCAAAGGAAAGAATG	ATCACATTCAGCTGGGGATCAAGATAGCCTTCTGGATCTTGAAGGAGAAGCTGGATTCCA	TTAGGTGAGGTTGAAGATGATGGGAGGTCTACACAGACGGAGCAACCATGCCAAGTAGGA 	GAGTATAAGGCATACTGGGAGATTAGAAATAATTACTGTACCCTTAACCCTGAGTTTGCGT 	AGCTATCACTCACCAATTATGCATTTCTACCCCCTGAACATCTGTGGTGTAGGGAAAAGA	GAATCAGAAAGAAGCCAGCTCATACAGAGTCCAAGGGTCTTTTGGGATATTGGGTTATGA 	TCACTGGGGTGTCATTGAAGGATCCTAAGAAAGGAGGACCACGATCTCCCTTATATGGTG	AATGTGTTGTTAAGAAGTTAGATGAGAGGTGAGGAGACCAGTTAGAAAGGCAATAAGCAT A THILLIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHI	TTCCAGATGAGAGATAATGGTTCTTGAAATCCAATAGTGCCCAGGTCTAAATTGAGATGG	GTGAATGAGGAAAATAAGGAAGAGAAGAGGGAAGATGTGCTGCTAGGTTTGTGATGCTGT	CTTTCCTGGGTCTTTGTCTCCACAGGAGCCATGGGGCACTACGTCTTAGCTGAACG	TGAGTGACACCCAGCCTGCAGACTCACTGTGGGAAGGAGCAAAACTAGAGACTCAAAGA	GGGAGTGCATTTATGAGCTCTTCATGTTTCAGGAGAGTTGAACCTAAACATAGAAATT 	GCCTGACGAACTCCTTGATTTTAGCCTTCTCTGTTCATTTCCTCAAAAGATTTCCCCAT	TTAGGTTTCTGAGTTCCTGCATGCCGGTGATCCCTAGCTGTGACCTCTCCCCTGGAACTG
6301	6361 6361	6421	6481	6541 6541	6601	6661	6721 6721	6781 6781	6841 6841	6901	6961 6961	7021	7081	7141	7201	7261 7261	7321 7321
Qy Db	Oy Dp	oy Dp	Qy Dp	Qy Db	Qy	QY	Qy Dp	OY Db	Qy	Oy Db	QY	Oy Dp	QY	Qy Db	Qy	Qy Db	Oy Dp

7440 7680 7680 7740 7800 7860 7860 7920 7980 8040 8100 8160 8160 8400 8400 8460 8460 8520 CATCTGATTGTGATGTGAGTTGCACAGCTATGAAGGCTGTACACTGCACGAATGGAAGAG AGGTAGGAGGCAAATATCTTGAAAGGGGTTGTGAAGAGGTGTTTTTTCTAATTGGCATGA AGGTGTCATACAGATTTGCAAAGTTTAATGGTGCCTTCATTTGGGATGCTACTCTAGTAT TCCAGACCTGAAGAATCACAATAATTTTCTACCTGGTCTCTCCTTGTTCTGATAATGAAA ATTATGATAAGGATGATAAAAGCACTTACTTCGTGTCCGACTCTTCTGAGCACCTACTTA CATGCATTACTGCATGCACTTCTTACAATAATTCTATGAGATAGGTACTATTATCCCCAT ACGCCTGTAGTCCCAGCTACTCGGAAGGCTGAGGCAGGAGAATGGCATGAACCCAGGAGG 8461 IAGAGTATCTCATAGTTTGTCAGTGATAGAAACAGGTTTCAAACTCAGTCAATCTGACCG CTTACATGATTCATTTTAACATCTGAGAAAAGCTTTGAACCCTGGGACGTGGCTAGTCAT **AACCTTACCAGATTTTTACACATGTATCTATGCATTTTCTGGACCCGTTCAACTTTTCCT** TTGAATCCTCTCTCTGTGTTACCCAGTAACTCATCTGTCACCAAGCCTTGGGGATTCTTC GCACCTGTCCCAGAAAAAGCATCATGGCTATCTGTGGGTAGTATGATGGGTGTTTTTAGC AGCACTITIGGGAGGCCAAAGCGGGTGGATCACGAGGTCAGGAGATCGAGACCATCCTGGC TAACATGGTGAAACCCCCATCTCTAATAAAAATACAAAAATTAGCTGGGCGTGGTGGCAG CAGAGCTTGCAGTGAGCCGAGTTTGCGCCACTGCACTCCAGCCTAGGTGACAGAGTGAGA 7741 7381 7501 7501 7561 7561 7621 7621 7681 7681 7741 7801 7801 7861 1861 7921 7921 7981 7981 8041 8101 8161 8221 8221 8281 8341 8401 7381 8041 8101 8161 8281 8341 8401 q g Ω QQ Dp οy QΥ Ω QΛ ò QQ οy g ΩŸ Q οy g QΥ qq QΥ QQ δy CD δy Q QΥ Op οy g Ω a δ Ω Ωý a ΩŽ

	rctcagacaccactacattcagtagtttagatgcctacaataaata	GGCTCTTCTCTTGTCTCATTGTTTCTTCTGAGTGAGCTTGAATCACAT 8640 	GCAGAAAACAACCAACTGATCCTCAGCTGTCA 	STCCTGGAATGTGACTCCCTTGCTCCTCT 	CCTACGCAAGGACTGTAATTGGTGGGGAC 	GTGTCCTCCCTAGGCCAGTGCCTCTGGAGTCAGAACTC 	3TGGAGTAAGCTCTCTCATTTTGAG 	rGCCCAGGTCCTTCCATGGAGCCACT 	ZAGGACATTCAGGAATTGCTAGATTCTGGGA 	TTTTTTTTTTGCCCTATGCCCCAGG 	CTGTAACCTCTGCCTCCCAGGTTCAAGGGATTCTCCT 	GATTACAGGCGTGCACCACCATGCCCGGCTAN 	CACCATGTIGGCCAGGCTGGTCTCGAACTCT 	CTCCCAAGTGCTGAGATTACAGGT 	NATATATCCAGATGGCATGTGTTTAC 	rGTGGTACAAGCATTCTGTCTTG 	AAGTTTCTTTAGGCATTAAATTTTAGCAAAGATATCTC 	ITCTTTTTTGTGGTTAGAAAGTTATGTAGAAAAAAGTAAATGTGA
 atagt	rcAG tcag	GCTCTT gctctt	CAG 	SCT	TCTTTGGACCCTAC 	rGTCC tgtcc	rGGAGT tggagt	rGCCCAG Egcccag	AGGA agga	rrrr 	CTCACTGTAAC	raca IIII Eaca	ACCAT 	$\omega - \sigma$	AGTCTTAATATATAT 	STGGT gtggt	STTTC 	TTTCTT
8461	8521	8581	8641 (8701	8761	8821	8881 8	8941	9001	9061	9121	9181	9241	9301	9361	9421	9481	9541
qq	oy og	Oy Db	65 P	oy Op	ç d	Q P	o P	6 6	Q Pb	Oy Dp	Q P	S G	Q P	Q P	Oy Dp	Q Q	Qy Db	δ

10440 10140 10500 10560 10020 10080 10140 10200 10260 10260 10380 10380 10500 10620 10620 10020 10080 10320 10440 10560 9600 9780 0066 0066 0966 0966 CATTCTGAAAGCATATGACAAATTATTTCTCTCTTAATATCTTACTATACTGAAAGCAGA CTATTTGAATTGCTGGAATCACAGGCCATTGCTGAGCTGCCTGAACTGGGAACACAAAG ttaaaccattttttttttgtggttagaaagttatgtagaaaaaagtaaatgtgattt AGGTAAGCATTTGTTTTATATTGGTTTTTTTTCACCTGGGCTGAGATTTCAAGAAACACC TITITCTGGCTTTATTCATAAATTCTTAAGGTCAACTACATTTGAAAAATCAAAGACCTG CATITITAAATICITATICACCICIGGCAAAACCATICACAAACCATGGTAGTAAAGAGAA TATACTITAATAAATGTATATTGTATTGTATACTGCATGATTTTATTGAAGTTCTTGTTC TCTTCACTCTAGGGACATTGTCGTCTAAGTTGTAAGACATTGGTTATTTTACCAGCAAAC TGAAAAACTATTAACAACTTGTCTATTACCTGTTAGTATTATTGTTGCATTAAAAATGCA CTITACATTTTGTCTTACGGAATATTTTCATTCAACTGTGGTAGCCGAATTAATCGTGTT <u> ACGCTCATTGTAGAAAAGCTATAAAATGAATACAATTAAAGCTGTTATTTAATTAGCCAG</u> 9541 9661 9781 9841 9901 9961 10141 10201 10261 10381 10441 10501 10561 10561 9601 9601 9661 9721 9721 9781 9841 9901 9961 10021 10201 10261 10381 10501 10021 10081 10081 10141 10321 10321 10441 qq Д q qq δ g δy Dp δλ g Qγ Op Ω q Ωÿ qq δλ q Q_{Y} g Qγ Db Qγ QQ οy qq QΥ qq Óγ g δ g ÓΫ Ω οy Qγ

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         10681 TGAGAGGTACAGGCCAAAATTCTTATGTTGTATTATAATAATGTCATCTTATAATACTGT 10740
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"G to A substitution (24d1 mutation
associated with HH), results in Cys
Tyr substitution"
                                                                                                                                                                                                                                                                           g "C to G substitution (24d2 mutation) results in His to Asp substitution"
                                                                                                                                                                                                                                                                                                      "A to T substitution (24d7 variant) results in Ser to Cys substitution'
                                                                                                                                  Hereditary haemochromatosis; metal toxicity; diagnosis;
                                                                                                                                       gene therapy; prenatal screening; human; ds
                                                                                                                                                        Location/Qualifiers 361.7147 / Atag a / Atag a / Note a 437.3761
                                               10801 TAAAATCCCCAAATTTTTCATAAAC 10825
                                                          10801 taaaatccccaaatttttcataaac 10825
                                                                                                                      Hereditary haemochromatosis gene.
                                                                                      BP.
                                                                                     AAT96690 standard; DNA; 10825
                                                     (MERC-) MERCATOR GENETICS INC.
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96US-0632673.
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                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                  WO9738137-A1
                                                                                                                                                                                                                                                                                                                                                                        04-APR-1997;
                                                                                                            14-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                   23-MAY-1996;
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16-APR-1996;
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                                                                                                                                                                                                                                                                                           variation
                                                                                                AAT96690;
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This genomic DNA sequence corresponds to the human gene whose mutated form is associated with hereditary haemochromatosis (HH).

To identify this novel gene, allelic association patterns were determined between known markers and the HH locus in the HHA region of chromosome 6. A physical clone coverage was then generated certending from D6S265, which is a marker that is centromeric of HLA-A, in a telomeric direction through D6S276, a marker at which the allelic association was no longer observed. A single mutation of (24d1) in the HH gene appears responsible for the majority of HH disease. This comprises a G to A substitution that is present in 68% of affected chromosomes and in 4% of unaffected chromosomes.

It results in a Cys to Tyr substitution in the encoded protein (see AAW36499) at a critical disulphide bridge important for secondary structure. The following are claimed: the HH genomic DNA (1), a 1437 bp cDNA sequence (Ia) (see AAT96691) and their 24d1, 24d2 and 24d7), or a peptide of at least 56 amino acid contact chosen from the HH gene product, its variants (24d1, 24d2 and 24d7), or a peptide of at least 56 amino acid contactions an antibody produced using the peptide; a method contaction, an animal model for the HH disease, metal chelation contaction, an animal model for the HH disease, metal chelation contaction with HH disease; an ethicactic agents for the mitigation of injury due to oxidative process in vivo or the mitigation of inconverload; a method for screening potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCAGGATTTAAAAACCAAGGGGGACACTGGATCACCTAGTGTTTCACAAGCAGGTACCTT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTACTGGGCATCTCCTGAGCCTAGGCAATAGCTGTAGGGTGACTTCTGGAGCCATCCCCG 300
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                                                                                                                                                                                                                Hereditary haemochromatosis gene and variants - useful for diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antisence oligonucleotide directed against a transcriptional product of a nucleic acid sequence as above; and oligonucleotides or pairs of oligonucleotides covering a range of nucleotides from (1), (1a) or their variants, useful for detecting a polymorphism in the HH gene. The invention also relates to methods for screening for HH homozygotes, to HH diagnosis, prenatal screening and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTGCTGTAGGAGAGAGAGAACTAAAGTTCTGAAAGACCTGTTGCTTTTCACCAGGAAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TCTAAGGTTGAGATAAAATTTTTAAATGTATGAATTGAAATTTTGAAAATCATAAATATTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 10825 BP; 2996 A; 2254 C; 2648 G; 2927 T; 0 other;
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       Thomas WJ;
                                                                                                                                                                                                                                                     and treatment of hereditary haemochromatosis disease
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   Gnirke A, Ruddy D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 0;
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Matches 10819; Conservative
Drayna DT, Feder JN, Gni
Tsuchihashi Z, Wolff RK;
                                                                                                        WPI; 1997-512743/47.
                                                                                                                                             P-PSDB; AAW36499
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27	01 GCTGGGTGTGGTGGCAT
27	61 TTGCTTGAGCCCAGGAAGTTGAGGCTGCAGTGAGCCATGACTGTGCCACTGTACTTCAGC 2820
28	21 CTAGGTGACAGACAAGACCCTGTCTCCCCTGACC
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6780 0099 6720 6720 6780 0069 5940 0009 0009 0909 0909 6120 6120 6180 6180 6240 6300 6360 6420 6420 6480 6480 6540 0999 0999 GAATCAGAAAGAAGCCAGCTCATACAGAGTCCAAGGGTCTTTTGGGATATTGGGTTATGA TAGTACCTCTGCCCCAGGGCACAGTGGGAAGAGGGGCAGAGGGGGATCTGGCATCCATGGG TITGCAAGAGCTGTTTAAGGTAGTACAGGGGCTTTGAGGTTGAGAAGTCACTGTGGCTAT TCTCAGAACCCAAATCTGGTAGGGAATGAAATTGATAGCAAGTAAATGTAGTTAAAGAAG TTAGGTGAGGTTGAAGATGAGGAGGTCTACACAGACGGAGCAACCATGCCAAGTAGGA GAGTATAAGGCATACTGGGAGATTAGAAATAATTACTGTACCTTAACCCTGAGTTTGCGT AGCTATCACTCACCAATTATGCATTTCTACCCCTGAACATCTGTGGTGTAGGGAAAAGA TCACTGGGGTGTCATTGAAGGATCCTAAGAAAGGAGGACCACGATCTCCCTTATATGGTG AATGGTTCTCCCCAGAATGAAAGTCTCTAATTCAACAACAACATCTTCAGAGCACCTACTAT CCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAG CAGAGATATACGINCCAGGIGGAGCACCCAGGCCIGGAICAGCCCCTCATIGIGAICIGG TGAGGAGGTAATTATGGCAGTGAGATGAGGATCTGCTCTTTGTTAGGGGGTGGGCTGAGG GTGGCAATCAAAGGCTTTAACTTGCTTTTTTTTTTTAGAGCCCTCACGGTCTGGCACCC TGTTCATAATATTAAGGAAGAGGCAGGGTTCAAGTGAGTAGGAACAAGGGGGAAGTCTCT TAGTCATTGGAGTCATCAGTGGAATTGCTGTTTTTGTCGTCATCTTGTTCATTGGAATTT 5941 6181 6241 6241 6301 6301 6361 6361 6421 6481 6481 6541 6541 6601 6601 6661 1999 6721 6781 6841 5761 5761 5821 5821 5881 5881 5941 6001 6001 6061 1909 6121 6121 6181 6421 6721 6781 Op QQ g qq g δ g δy Db δλ PP Qy QQ Óγ q δy qq οy qq δý qq Qγ qq δý g QΥ Db δý g ò Op Qy δy QΥ δy Ω

6841 tcactggggttcattgaaggatcctaagaaaggagaccacg 6901 AANGTTGTTAGATCAAAGTAAAAAAACACAACAACAACAACAACAACAACAACAACAA
6841 tc 6901 ac 6901 ac 6901 ac 6901 ac 6901 ac 6901 ac 6901 ac 6901 pc 7021 gc 7021 g

8940 8760 8760 8820 8880 8880 8940 0906 8640 8700 8280 8340 8400 8400 8460 8460 8520 8580 8280 8100 8160 8220 8040 8100 8160 tecagacetgaagaateacaataattttetaeetggteteteettgttetgataatgaaa 7980 CCTGAAGGAAGGTCCTGGAATGTGACTCCCTTGCTCTTGTTGCTCTTTTGGCATTCA GCTTAGAGGATGCCCAGGTCCTTCCATGGAGCCACTGGGGTTCCGGTGCACATTAAAAAA GAAGGGGAACAGCAGAAAACAACCAACTGATCCTCAGCTGTCATGTTTCCTTTAAAAGTC ACGCCTGTAGTCCCAGCTACTCGGAAGGCTGAGGCAGGAGAATGGCATGAACCCAGGAGG TAGAGTATCTCATAGTTTGTCAGTGATAGAAACAGGTTTCAAACTCAGTCAATCTGACCG CAGAGCTTGCAGTGAGCCGAGTTTGCGCCACTGCACTCCAGCCTAGGTGACAGAGTGAGA AGCACTTTGGGAGGCCAAAGCGGGTGGATCACGAGGTCAGGAGATCGAGACCATCCTGGC CATGCATTACTGCATGCACTTCTTACAATAATTCTATGAGATAGGTACTATTATCCCCAT TTCTTTTTTAAATGAAAGTGAAGTAAGCCGGGCACGGTGGCTCACGCCTGTAATCCC 8881 9001 8701 8761 8761 8821 8821 8881 8941 8941 9001 8641 8281 8341 8401 8461 8461 8521 8521 8581 8641 8701 8341 8401 8101 8221 8281 8041 8041 8161 8161 8221 7921 7981 7981 8101 pp Dp g Qγ g QQ ò PP δ g QΥ g δy Db ÓΫ g δÿ οy Вb QΥ qq δλ g Qγ QQ Qγ Qγ qq QΥ g Qγ ŏ Db g οy Q

Qy 10141 CCAGTCTTCACAGTA	Qy 10201 GTTAATTTTTTAAT 	Oy 10261 TTTTCTGGCTTTAT 	10321	Oy 10381 GGGTGACACCTGGTG 	10441	10501	10561	10621	10681	10741	Qy 10801 TAAATCCCCAAATT 	RESULT 6 AAA96794 ID AAA96794 standard; c	X C AAA96794; X DT 19-FEB-2001 (first	Genomic L	major h chromos Homo sa	Key exon	FT intron /num FT intron /*ta FT /*ta FT exon 4652	
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10440 ACTCTCATAATCATGAGTCAAGTACAGGAGGTGATTGAGGACTGC 10680 AACACATTTCACTAACACATTACTAAACATCAGCAACTGTGGCCT 10200 10620 TAGAAATTTTAAGTCCTCATTTTCTTTCGGTGTTTTTTAAGCTTAA 10260 TTCATAAATTCTTAAGGTCAACTACATTTGAAAAATCAAAGACCTG 10320 PATTCACCTCTGGCAAAACCATTCACAAACCATGGTAATAAAGAGA 10380 attcacctctggcaaaaccattcacaaaccatggtagtaagagaga 10380 GGCCATAGGTAAATGTACCACGGTGGTCCGGTGACCAGAGATGCAG 10440 GGAATCACAGGCCATTGCTGAGCTGCCTGAACTGGGAACACAACAG 10620 CAAAATTCTTATGTTGTATTATAATGTCATCTTATAATACTGT 10740 ibility iron loading protein; HFE protein; bility complex; non-classical class I gene; n disorder; haemochromatosis; ss. stocompatibility iron loading (HFE) gene. ocation/Qualifiers .028..1324 /*tag= a /number= 1 /*tag= b /*tag= b /number= 1 4652..4915 TTTTCATAAAC 10825 CDNA; 12146 BP. t entry)

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The present sequence represents the human histocompatibility iron loading (HFE) gene. The HFE gene is a major histocompatibility (MHC) non-classical class I gene located on chromosome 6p. Mutations in the gene lead to iron disorders. The specification describes a method for diagnosing an iron disorder or a genetic susceptibility to develop the absorder in a mammal. The method comprises determining the presence of a mutation in exon 2 or an intron of a HFE gene or protein. The mutation is not a C to G missense mutation at nucleotide 187 of the sequence given in A96769 (Genbank Accession number U60319). The presence of the mutation indicates the disorder or the genetic susceptibility to the disorder. The method is used to diagnose an iron disorder e.g. haemochromatosis, or a genetic susceptibility to develop it.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Diagnosing an iron disorder e.g. hemochromatosis or a genetic susceptibility to develop it, by determining the presence of a mutation in exon 2 or an intron of a histocompatibility iron loading nucleic acid -
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Qy	4917	TGAAACCCGTCTCTAAAAAATACAAAATTAGCTGGTCACAGTCATGCGCACCTGTAGT 4976
QY	4977 5867	CCCAGCTAATTGGAAGGCTGAGGAGGAGGATCGCTTGAACCTGGGAAGCGGAAGGTTGCA 5036
Qy	5037 5927	CTGAGCCAAGATCGCGCCACTGCACTCCAGCCTAGGCAGCAGTGAGACTCCATCTTAA 5096
Qy Db	5097	50 44
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Qy	5337 6225	ATAAAGGGCAATTTTATCTATCAGAACAAGAACATGGGTAACAGATATGTATATACA 5396
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Qy	5457	ATGGTGTCTCCTGTAGCTTGTTTTTTTTTGAAAAGGGTATTTCCTTC 551

7376 7436 7496 8444 7676 7196 7256 7316 8384 8504 7076 7136 8144 8204 8264 8324 8564 9219 7664 9689 7784 7844 7016 7904 7964 8024 7484 GGGACTTACATGATTTTAACATCTGAGAAAAGCTTTGAACCCTGGGACGTGGCTAG TCATAACCTTACCAGATTTTTACACATGTATCTATGCATTTTCTGGACCCGTTCAACTTT GCATTICCAGATGAGAGATAATGGTTCTTGAAATCCAATAGTGCCCCAGGTCTAAATTGAG AACGTGAGTGACACGCAGCCTGCAGACTCACTGTGGGAAGGAGACAAAACTAGAGACTCA AAGAGGGAGTGCATTTATGAGCTCTTCATGTTTCAGGAGAGAGTTGAACCTAAACATAGA AATTGCCTGACGAACTCCTTGATTTTAGCCTTCTCTGTTCATTTCCTCAAAAAGATTTCC CCATITAGGITICTGAGTICCTGCATGCCGGTGATCCCTAGCTGTGACCTCTCCCCTGGA ATGGGTGAATGAGGAAAATAAGGAAGAGAGAAGAGGCAAGATGGTGCCTAGGTTTGTGAT **AAGAGAATCAGAAAGAAGCCAGCTCATACAGAGTCCAAGGGTCTTTTGGGATATTGGGTT** aatgatcacattcagctggggatcaagatagccttctggatcttgaaggagaagctggat **AGGAGAGTATAAGGCATACTGGGAGATTAGAAATAATTACTGTACCTTAACCCTGAGTTT** GCGTAGCTATCACTCACCAATTATGCATTTCTACCCCCTGAACATCTGTGGTGTAGGGAA TCCATTAGGTGAGGTTGAAGATGATGGGAGGTCTACACAGACGGAGCAACCATGCCAAGT 8445 8385 8025 8085 8145 8205 7377 8265 7437 8325 7497 7557 7017 7965 71197 7257 7425 7545 7605 6777 7665 6837 7725 6897 7785 6957 7845 7905 7077 7137 7317 6597 7485 6657 6717 g g q Db q QQ pp g QΥ Op ò g òλ qq ò g δ g δ qq οy αq Qγ 9 δý g Qγ g οy ò Ω Qγ Qγ QYò οy

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7 CTTCCATCTGATTGTGAGTTGCACAGCTATGAAGGCTGTACACTGCACGAATGGA 	7 AGAGGCACCTGTCCCAGAAAAAGCATCATGGCTATCTGTGGGTAGTATGATGGTGTGTTT	7 TAGCAGGTAGGAGGAAATATCTTGAAAGGGGTTGTGAAGAGGTGTTTTTCTAATTGGC 	7 ATGAAGGIGICATACAGAITIGCAAAGIITIAAIGGIGCCTICAITIGGGAIGCIACTICA	7 GTATTCCAGACCTGAAGAATCACAATAATTTTCTACCTGGTCTCTCCTTGTTCTGATAAT	7 GAAAATTATGATAAGGATGATAAAGGACTTACTTGGTGTCCGACTCTTCTGAGCACCTA	7 CTTACATGCATTACTGCATGCACTTCTTACAATAATTCTATGAGATAGGTACTATTATCC	7 CCATTICITITIAAAIGAAGAAGAGGGGGGGCGGGCAGGGGGGCTCAGGCCTGTAA 	7 TCCCAGCACTTTGGGAGGCCAAAGCGGGTGGATCACGAGGTCAGGAGATCGAGACCATCC	7 TGGCTAACATGGTGAAACCCCATCTCTAATAAAATACAAAAATTAGCTGGGCGTGGTG	7 GCAGACGCCTCTAGTCCCAGCTACTCGGAAGCTGAGGCAGGAGAGGAATGGCATGAACCCAG	7 GAGGCAGAGCTTGCAGTGAGCCGAGTTTGCGCCACTGCACTCCAGCCTAGGTGACAGAGT 	CTCAA ctcaa	7 AGTATAGAGTATCTCATAGTTTGTCAGTGATAGAAACAGGTTTCAAACTCAGTCAATCTG 	7 ACCGTTTGATACATCTCAGACACCACTACATTCAGTAGTTTAGATGCCTAGAATAAGTGC	7 AGAAGGAAGGAGATGGCTCTTCTCTTGTCTCATTGTGTTTCTTCTGAGTGAG	7 ACATGAAGGGGAACAGCAGAAAACAACCAACTGATCCTCAGCTGTCATGTTTCCTTTAAA	7 AGTCCCTGAAGGAAGGTCCTGGAATGTGACTCCCTTGCTCCTCTGTTGCTCTTTTGGCACTTGTTTGT
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10124 10184 10544 10304 10364 10724 9116 9236 9326 9416 9476 10424 9116 9704 9026 9236 9656 9886 TICATITCITIGGACCCTACGCAAGGACTGTAATIGGTGGGGACAGCTAGTGGCCCTGCT AAAAAAATCTAACCAGGACATTCAGGAATTGCTAGATTCTGGGAAATCAGTTCACCATG TICAAAAAGAGICTITITITITITITITAGACTCTATIGCCCAGGCTGGAGTGCAATGGCA CCCAAGTAGCTGGGATTACAGGCGTGCACCACCATGCCGGGCTAATTTTTGTATTTTAG TAGAGACAGGGTTTCACCATGTTGGCCAGGCTGGTCTCGAACTCTCCTGACCTCGTGATC CGCCTGCCTCGGCCTCCCAAAGTGCTGAGATTACAGGTGTGAGCCACCCTGCCCAGCCGT CAAAAGAGTCTTAATATATATATCCAGATGGCATGTTTACTTTATGTTACTACATGCA CCAGTGAAAAACTTAACAACTTGTCTATTACCTGTTAGTATTATTGTTGCATTAAAAA TGCATATACTTTAATAAATGTATATTGTATTGTATACTGCATGATTTTATTGAAGTTCTT ATTICITIACATITIGICITACGGAATATITICATICAACIGTGGGTAGCCGAATTAATCG TTTCCCTCAATGAAGTGGAGTAAGCTCTCTCATTTTGAGATGGTATAATGGAAGCCACCA AGTGGCTTAGAGGATGCCCAGGTCCTTCCATGGAGCCACTGGGGTTCCGGTGCACATTAA TCTTTTAAAACCATTTTCTTTTTTTGTGGTTAGAAAAGTTATGTAGAAAAAAGTAAATGTG GTTCATCTTGTGTATATACTTAATCGCTTTGTCATTTTGGAGACATTTTTGCTTCTA 9645 9765 9825 9177 10185 9417 9477 10425 9597 8757 8817 9705 8877 8937 8997 9885 9057 9945 9117 10005 9237 10125 9297 9357 9537 9657 9717 9837 10245 10305 10365 9777 10065 10485 10545 10605 10665 QQ g qq qq QQ Ωp QQ Dp g Qγ Dp δy δ qq QΥ δ Qγ QΥ δy Qγ g qq qq Ω q q δ Ω QΥ Qγ q QΫ Pp δy Ω δ (first

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The present invention describes hereditary haemochromatosis gene products from the human haemochromatosis gene. The present sequence represents a hereditary haemochromatosis subregion from an hereditary haemochromatosis subregion from an hereditary haemochromatosis with a presence or absence of the common hereditary haemochromatosis (HFE) gene mutation in an individual comprising:

Cap providing DNA or RNA from the individual; and (b) assessing the DNA or RNA for the presence or absence of the haplotype genotype indicates the likely presence or absence of the haplotype genotype indicates the likely presence of the HFE gene mutation in the genome of the individual. The HFE gene sequences from the present invention can be used to develop products for use in the diagnosis and treatment of HFE. The present protein butyrophilin (FF), and can be used in the production of agonists of and antagonists of BY function. Also described are: (1) a RoRet gene which are homologues of the milk products for use in the broadces for the study, diagnosis and treatment of lugues and Slogren's syndrome; and (2) NFT3 and can can be used to develop products for the study, diagnosis and treatment of lugues and Slogren's syndrome; and (2) NFT3 and can can be used to develop products for the study, diagnosis and can be used to develop products for the study, also which are homologues of a type 1 sodium transport gene, and can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bovine butyrophilin; BT; human hereditary haemochromatosis; HFE; diagnosis; iron metabolism; NPT3; NPT4; RORet; BTF1; BTF2; BTF3; BTF4; BTF5; milk protein; lupus; Sjogren's syndrome; hypophosphatemia;
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                                                  Hereditary haemochromatosis subregion from an HH affected individual
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for the diagnosis and treatment of hereditary disorders in
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Best Local Similarity 99.5%;
Matches 10779; Conservative
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Qy Db	301	TTTCCCGCCCCCAAAAGAAGCGGAGATTTAACGGGGACGTGCGGCCAGAGCTGGGGAA 360
Qy Db	361	ATGGGCCGCGGAGCCAGGCCGGCGCTTCTCCTCCTGATGCTTTTGCAGACCGCGGTCCTG 420
QY	421	CAGGGCGCTTGCTGCGTGAGTCCGAGGCTGCGGGCGAACTAGGGGCGCGGGGGGGG
Qy Db	481	GAAAAATCGAAACTAGCTTTTTCTTTGCGCTTGGGAGTTTGCTAACTTTGGAGGACCTGC 540
Qy Db	541 46561	TCAACCCATCGGGAAGCCCCTCTCCCTACTTTCTGCGTCCAGACCCCGTGAGGGAGG
Qy Dp	601 46501	CTACCACTGAACTGCAGATAGGGGTCCCTCGCCCAGGACCTGCCCCCTCCCCCGGCTGT 660
07 Dp	661	CCGGGCTCTGCGGAGTGACTTTTGGAACCGCCCACTCCCCTTCCCCCAACTAGAATGCTTT 720
Qy Db	721	TAAATAAATCTCGTAGTTCCTCACTTGAGCTGAGCCTGGGGGCTCCTTGAACCTGG 780
Qy Dp	, 781 , 46321	AACTCGGGTTTATTTCCAATGTCAGCTGTGCAGTTTTTTCCCCAGTCATCTCCAAACAGG 840
QY Db	841	AAGTICTTCCCTGAGTGCTTGCCGAGAAGGCTGAGCAAACCCACAGCAGGATCCGCACGG 900
Qy Db	901	GGTTTCCACCTCAGAACGAATGCGTTGGGCGGGGGGCGCGAAAGAGTGGCGTTGGGGA 960
Qy Db	961	TCTGAATTCTTCACCATTCCACCCACTTTTGGTGAGACCTGGGGTGGAGGTCTCTAGGGT 1020
Qy Db	1021	GGGAGGCTCCTGAGAGAGCCTACCTCGGGCCTTTCCCCACTCTTGGCAATTGTTCTTT 1080
Qy Db	1081	GCCTGGAAAATTAAGTATATGTTTTGAACGTTTGAACTGAACAATTCTCTTTTCGG 1140
Qy Db	1141 45961	CTAGGCTTTATTGATTTGCAATGTGCTGTGTAATTAAGAGGCCTCTCTACAAAGTACTGA 1200
Qy Dp	1201	TAATGAACATGTAAGCAATGCACTCACTTCTAAGTTACATTCATATCTGATCTTATTTGA 1260
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44943 44823 45242 45122 45003 44883 45362 45063 2100 2160 1440 1740 1800 1860 2040 2340 2400 AATAAGAATGATATTGACTGGGAGCAGTATTTCCCAGGCAAACTGAGTGGGCCTGGCAAG 1980 ACAGTGATCTGTCACAGGCTTTTAAAAGATTGCTCTGGCTGCTATGTGGAAAGCAGAATG GCCACAAACAAGGTTGTGCAGGCGCCTGTAGGCTGTGGTGTAATTCTAGCCAAGGAGTA TATGATTCTTAAACATCACACTGCATTAGAGGTTGAATAAAAAATTTCATGTTGAGCAG TGTAGCACAGTGTTCTGTGGGGTCACACGCCGGCCTCAGCACAGCACTTTGAGTTTTGGTA CTACGTGTATCCACATTTTACACATGACAAGAATGAGGCATGGCACGGCCTGCTTCCTGG CAAATTTATTCAATGGTACACTGGGCTTTGGTGGCAGAGCTCATGTCTCCACATTCATAGC CAAGGGAGAGAGCAGGGAAACAAGTCTTTACCCTTTGATATTTTGCATTCTAGTGGGAGA GAAGCAGAGAAGTCAGGGCAAGTCACTCTGGGGCTGACACTTGAGCAGAGACATGAAGGA CCTCCCTACTCACTAGGTGCTAGGAGCACTCCCCCAGTCTTGACAAAAATGTCTCT AAACTTTGCCACATGTCACCTAGTAGACAAACTCCTGGTTAAGAAGCTCGGGTTGAAAAA AATAAACAAGTAGTGCTGGGGAGTAGAGGCCAAGAAGTAGGTAATGGGCTCAGAAGAGA GATGACAATAAGCAAATGAGCAGAAAGATATACAACATCAGGAAATCATGGGTGTTGTGA 45781 1681 45421 1801 1861 1921 45121 2041 2221 2281 44822 2341 1321 1381 1441 1501 1561 1621 45481 1741 45241 1981 2101 2161 45601 45541 45301 45181 45062 45002 44942 44882 45841 45721 45661 g qq QQ ρp a Db Db g ρp qq g g QQ g q Qγ g QY g Op δ ŏ δ ŏ δy δ δλ δŻ Qγ QY ōλ Qγ δý ŏ QΥ Qγ

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43444 43264 43204 43084 42964 42904 42844 42664 43384 43324 43024 42604 42784 3776 4016 4076 4316 4376 4436 4496 3656 3716 3836 3896 3956 4136 4196 4256 ACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCTTTGAAGCTTTGG TTTCATGCATCTTGAAGGAAACAGCTGGAAGTCTGAGGTCTTGTGGGGAGCAGGGAAGAGG GGATCTGGGGGCAGTGAGGGGGGTGGCAGCCACGTGTGGCAGAAAAGCACACAAGGAAA GAGCACCCAGGACTGTCATATGGAAGAAGACAGGACTGCAACTCACCTTCACAAAATG AGGACCAGACACACTGATGCTATGAGTTGATGCAGGTGTGTGGAGCCTCAACATCCTGC TCCCCTCCTACTACACATGGTTAAGGCCTGTTGCTCTGTCTCCAGGTTCACACTCTCTGC GCTACGTGGATGACCAGCTGTTCGTGTTCTATGATNATGAGAGTCGCCGTGTGGAGCCCC TGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTATGGAAAATCACAACC TGGGCAGGACCACCTTGAATTCTGCCCTGACACACTGGATTGGAGAGCAGCAGAACCCAG GGCCTGGCCCCACCAAGCTGGAAAGGCACAAGATTCGGGCCAGGCAGAACAGGGC CTACCTGGAGAGGGACTGCCCTGCACAGCTGCAGTTGCTGGAGCTGGGGAGAGTGT GAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGCAGCTGAGTCAGAGTC ACAGCAAGGGTATGTGGAGAGGGGGCCTCACCTTCCTGAGGTTGTCAGAGCTTTTCATCT GAAGGAATTTGCTTCCTGAGATCATTTGGTCCTTGGGGATGGTGGAAATAGGGACCTATT CCTTTGGTTGCAGTTAACAAGGCTGGGGATTTTTCCAGAGTCCCACACCCTGCAGGTCAT CCTGGGCTGTGAAATGCAAGAAGACAACAGTACCGAGGGCTACTGGAAGTACGGGTATGA 3537 3597 3657 3717 3777 3837 3957 4017 43083 4077 4257 4317 4377 4437 4497 3477 3897 4137 4197 42723 43623 43563 43503 43443 43383 43323 43263 43203 43143 43023 42963 42903 42843 42783 42603 42663 pp qq Dp QQ δý Op δ qq qq g qq qq Q qq qq q qq g g Db ŏ Dp δλ οχ δý οy Qγ Qγ Ωý Ω Qγ Óγ δ $\dot{\Omega}$ Qγ οy

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40926 40806 41286 41106 40746 41046 6356 6416 6476 6536 9219 6116 9/19 6296 5816 5876 AATGATCACATTCAGCTGGGGATCAAGATAGCCTTCTGGATCTTGAAGGAGAAGCTGGAT **AGGAGAGTATAAGGCATACTGGGAGATTAGAAATAATTACTGTACCTTAACCCTGAGTTT** GCGTAGCTATCACCAATTATGCATTTCTACCCCCTGAACATCTGTGGTAGGGAA TCCATTAGGTGAGGTTGAAGATGATGGGAGGTCTACACAGACGGAGCAACCATGCCAAGT CTATTTTGCAAGAGCTGTTTAAGGTAGTACAGGGGCTTTGAGGTTGAGAAGTCACTGTGG ATTTTGTTCATAATATTAAGGGAAGGCAGGGTTCAAGTGAGTAGGAACAAGGGGGAAGT CTCTTAGTACCTCTGCCCCAGGGCACAGTGGGAAGAGGGGCAGAGGGGATCTGGCATCCA TGGGAAGCATTTTTTTTTTTTTTTTTTGGGGACACCAGCAGCTCCCTGGGAGACAGA ATTGCCCAATGGGGATGGGACCTACGAGGCTGGATAACCTTGGCTGTACCCCCTGGGGA ATTGCCCAATGGGGATGGGACCTACAGGGCTGGATAACCTTGGCTGTACCCCCTGGGGA AGAGCAGAGATATACGTNCCAGGTGGAGCACCCAGGCCTGGATCAGCCCCTCATTGTGAT CTGGGGTATGTGACTGATGAGAGCCAGGAGCTGAGAAAATCTATTGGGGGTTGAGAGGAG TGCCTGAGGAGGTAATTATGGCAGTGAGATGAGGATCTGCTCTTTGTTAGGGGGTGGGCT 6717 40985 6177 6357 40445 6237 6297 6417 6477 6537 6657 40865 40685 40625 40565 41465 5757 5817 41285 5877 5937 5997 41105 6057 41045 6117 40925 40805 40745 5697 41345 41225 41405 g Dp g g Öλ q g g δy δ Q ŏ QΥ δ a g Qγ g δλ g QΥ g δy g Ω d $^{\circ}$ g qq Db Ωy d Ω δ óλ Qγ

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Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibaterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardivoxscular disorder; neurological disease; infection; human; secreted protein;
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                                                                                                                                                                                                       GCAGCGCTGAGGGTTTCCTGAAGGTAAAGAATAAAGAATAAGGTGGAGGGGCGTGCACT
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Homo sapiens
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SM, Barash SC, CA, Rosen

WPI; 2001-451937/48

Isolated polypeptide for treating, preventing and or prognosin disorders related to the musculoskeletal system including musculoskeletal cancers and also for testing and detection e.g. diagnosis

English. Listing; Sequence + NO 3112; 781pp SEQ ID Example 2;

The invention relates to novel genes (AAL34669-AAL37666) and proteins (ABB03087-ABB04109) associated with the musculoskeletal system useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (antisqualists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and prevention of: (a) cancer, e.g. breast and ovarian cancer and coher cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune tract, liver, lung, or urogenital; (b) immune concerns of sisease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple scalerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as mycoradial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences. parasitic infections.

BP; 1600 A; 1192 C; 1403 G; 1553 T; 1 other; Sequence 5749

ij 4240 4180 4300 4480 4120 ATGGAAAATCACAACCACAGGGTATGTGGAGGGGGGCCTCACCTTCCTGAGGTTG 4060 AGCTGGGGAGAGGTGTTTTGGACCAACAAGGTATGGTGGAAACACACTTCTGCCCCTATA 4540 GGAAGTACGGGTATGATGGGCAGGACCACCTTGAATTCTGCCCTGACACACTGGATTGGA 4360 GAGCAGCAGAACCCAGGGCCTGGCCCACCAAGCTGGAGTGGGAAAGGCACAAGATTCGGG 4420 tcagagcttttcatcttttcatgcatcttgaaggaaacagctggaagtctgaggtcttgt 120 acaccetycaggtcatcetgggetgtgaaatgeaagaagacaacagtaccgagggetact 300 480 420 9 Gaps TCAGAGCTTTTCATCTTTCATGCATCTTGAAGGAAACAGCTGGAAGTCTGAGGTCTTGT GGGAGCAGGAAGGAAGGAATTTGCTTCCTGAGATCATTTGGTCCTTGGGGATGGTG GAAATAGGGACCTATTCCTTTGGTTGCAGTTAACAAGGCTGGGGATTTTTCCAGAGTCCC ACACCTGCAGGTCATCCTGGGCTGTGAAATGCAAGAAGACAACAGTACCGAGGGCTACT gagcagcagaacccagggcctggcccaccaagctggagtgggaaaggcacaagattcggg CCAGGCAGAACAGGGCCTACCTGGAGGGACTGCCCTGCACAGCTGCAGCTGCTGG ccaggcagaacagggcctacctggagagggactgccctgcacagctgcagcagttgctgg DB 22; Length 5749; Indels 6; 52.9%; Score 5724.8; ilarity 99.8%; Pred. No. 0; Conservative 0; Mismatches Similarity Query Match Best Local Simi Matches 5740; 4001 4181 4061 61 4121 4241 241 4301 301 4421 4481 121 181 4361 361 421 ď g g g g g g g g ò ò ò δ δ ò δ

4720 TGTATATTTATACCTGTTAAAAATTCAGAAATGTCAAGGCCGGGCACGGTGGCTCACCCC 4840 agctgggggagaggtgttttggaccaacaaggtatggtggaaacacattctgcccctata TGGCTGAGGCTGTGTCCTCTCCAAATTCTGGGAAGGGACTTTCTCAATCCTAGAGTCTC TACCITATAATTGAGATGTATGAGACAGCCACAAGTCATGGGTTTAATTTCTTTTCTCCA CATGCGCACCTGTAGTCCCAGCTAATTGGAAGGCTGAGGCAGGAGCATCGCTTGAACCTG CTCTAGTGGCAGAGGAGGAGGTTGCAGGGCACGGAATCCCTGGTTGGAGTTTCAGAGG tgtatattttatacctgttaaaaattcagaaatgtcaaggccgggcacggtggctcaccct a-gttaaaagtttctttcatagnacatagcaataatcactgaagctacctatcttacaag TGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGTGGTCACAAGGTCAGGAGTTTGAGACC AGCCTGACCAACATGGTGAAACCCGTCTCTAAAAAAATACAAAAATTAGCTGGTCACAGT GGAAGCGGAAGTTGCACTGAGCCAAGATCGCGCCACTGCACTCCAGCCTAGGCAGCAGAG TGAGACTCCATCTTAAAAAAAAAAAAAAAAAAAAAAAAGAATTCAGAGATCTCAGCTAT AGGTTAAAAAGTTTCTTTCATAGAACATAGCAATAATCACTGAAGCTACCTATCTTACAAG TCCGCTTCTTATAACAATGCCTCCTAGGTTGACCCAGGTGAAACTGACCATCTGTATTCA ATCATTTTCAATGCACATAAAGGGCAATTTTATCTATCAGAACAAAGAACATGGGTAACA CATATGAATACCAGGACAAAATATCAAGTGAGGCCACTTATCAGAGTAGAAGAATCCTTT TGTTAGAGTCCAATCTTAGGACACAAAATGGTGTCTCTCCTGTAGCTTGTTTTTTTCTGA **AAAGGGTATTTCCTTCCTCCAACCTATAGAAGGAAGTGAAAGTTCCAGTCTTCCTGGCAA** GGGTAAACAGATCCCCTCTCTCCTTCCTTTCCTGTCAAGTGCCTCCTTTGGTGA 4661 1081 5141 1141 1260 1320 4721 721 4781 4841 841 4901 4961 5021 1021 5081 5201 1201 5261 5321 5381 1380 1440 5501 5561 661 781 901 961 g g Ωy δy Db QΥ ò g g g 엄 Ω ŏ Qγ Dp Ω g δ QQ δy qq Dp QΥ Qγ pp δy g δy g QY g ρ g ΟŻ g Qγ

CT 5680 1679 5740	t 173	GG 5800 99 1799	TC 5860 tc 1859	AT 5920 at 1919	TT 5980 tt 1979	GA 6040 ga 2039	sr 6100 2099	TA 6160 ta 2159	3A 6220 ga 2219	AG 6280 ag 2279	AAC 6340 aac 2339	GT 6400 gt 2399	CA 6460 ca 2459	TA 6520 ta 2519	TT 6580 tt 2579	3G 6640 	TA 6700 ta 2699
TCGGGCCTTGAACT tcgggccttgaact	aatggatgccaa	GGGCTGGATAACCTT 	GCACCCAGGCCTGGA 	GAGCTGAGAAAATCT 	GATGAGGATCTGCTC 	rGCTTTTCTGTTTTA 	AATTGCTGTTTTTGTC 	GCAGGGTTCAAGTGAG 	NGTGGGAAGAGGGGCA 	CTTTGGGGACACCAGC 	GTCTCTAATTCAACAA 	GTACAGGGGCTTTGAG 	GGAATGAAATTGATAG 	GCAGGAAGCAAATGCT gcaggaagcaaatgct	GATAGCCTTCTGGATC 	GGAGGTCTACACAGAC 	TTAGAAATAATTACTG ttagaaataattactg
GACCACTCTACGGT 	gaaggataagcag	GGGATGGGACCTACCA 	ATACGTNCCAGGTGGA 	GACTGATGAGAGCCAG 	GTAATTATGGCAGTGA 	TCAAAGGCTTTAACTT 	TGGAGTCATCAGTGGA 	AATATTAAGGAAGAGG 	TCTGCCCCAGGGCACA(TTTCTCATTTATATT 	CTCCCCAGAATGAAAC 	SAGCTGTTTAAGGTA 	ACCCAAATCTGGTAGG 	GAGGTCCTAAAGCAG(TCAGCTGGGGATCAA 	AGGTTGAAGATGATG aggttgaagatgatg	AGGCATACTGGGAGA aggcatactgggaga
TGTGACCTCTTCAG	caccatgaagt	CGTATTGCCCAATG 	GGAAGAGCAGAGAT 	GATCTGGGGTATGT 	3GAGTGCCTGAGGAGG 	GGCTGAGGGTGGCAAT 	TGGCACCCTAGTCAT1 	GGAATTTGTTCAT 	AGTCTCTTAGTACC 	TCCATGGGAAGCATT 	CAGAAATAATGGTTC 	CCTACTATTTGCAA(GTGGCTATTCTCAGA) 	TAAAGAAGACCCCAT(taaagaagacccat	AAAGAATGATCACAT' 	GGATTCCATTAGGTG ggattccattaggtg;	AAGTAGGAGAGTATAJ
GGTGACACATC ggtgacacatc		TCGAACCTAAAGA tcgaacctaaaga	CTGTACCCCCTGG	AGCCCCTCATTGT 	TGGGGGTTGAGAG tgggggttgagag	TGTTAGGGGGTGC 	GCCCTCACCGTCT 	CATCTTGTTCATT	GGAACAAGGGGGAI 	GGGGATCTGGCAT 	CTCCCTGGGAGAC 	ATCTTCAGAGCA 	TGAGAAGTCACT tgagaagtcact	AGTAAATGTAGT agtaaatgtagt	GGGTGTCAAAGG gggtgtcaaagg	GAAGGAGAAGCT 	AGCAACCATGCC.
5621 1620 5681	9 9	5741	5801	5861	5921 1920	5981	6041	6101	6161	6221	6281	6341	6401	6461	6521	6581	6641
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7540 7240 7300 7480 7600 3599 7720 7180 7360 7420 3419 3179 6760 6880 2999 7060 3059 7120 3119 GTATGATGGGTGTTTTTAGCAGGTAGGAGGCAAATATCTTGAAAGGGGTTGTGAAGAGGT CCTCAAAAAGATTTCCCCCATTTAGGTTTCTGAGTTCCTGCATGCCGGTGATCCCTAGCTG CCTGGGACGTGGCTAGTCATAACCTTACCAGATTTTTACACATGTATCTATGCATTTTCT GGACCCGTTCAACTTTTCCTTTGAATCCTCTCTGTGTTACCCAGTAACTCATCTGTCA CCAAGCCTTGGGGATTCTTCCATCTGATTGTGATGTGAGTTGCACAGCTATGAAGGCTGT CCAGGTCTAAATTGAGATGGGTGAATGAGGAAAATAAGGAAGAGAGAAAAAGAGAGATGG TGCCTAGGTTTGTGATGCCTCTTTCCTGGGTCTCTTGTCTCCACAGGAGGAGCCATGGGG CAAAACTAGAGACTCAAAGAGGGAGTGCATTTATGAGCTCTTCATGTTTCAGGAGAGAGT TGAACCTAAAACATAGAAATTGCCTGACGAACTCCTTGATTTTAGCCTTCTCTGTTCATTT GTTAGAAAGCCAATAAGCATTTCCAGATGAGAGATAATGGTTCTTGAAATCCAATAGTGC 3600 7721 7781 3180 3240 7361 3420 7481 3480 7541 3540 7601 7661 3660 3720 2820 3120 7241 7301 3300 3360 7421 2760 2880 6941 2940 7001 3000 1907 3060 7121 7181 6701 1949 6821 6881 2700 g g g qq Qγ qq δy g οy P Ωÿ g οy DP QY g Qy Db Qy Db δ ВÞ δ g Qγ g ò g Ω ρp οy g δy Ω á δ ò

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	GTTTTTTCTAATTGGCATGAAGGTGTCATACAGATTTGCAAAGTTTAATGGTGCCTTCAT	TTGGGATGCTACTTACTAGATTCCAGACCTGAAGAATCACAATAATTTTTTACTACCTGGTCTC	TCCTTGTTCTGATAATGAAAATTATGATAAGGATGATAAAAGCACTTACTT	CTCTTCTGAGCACCTACTTACATGCATTACTGCATGCATG	ATAGGTACTATTATCCCCATTTCTTTTTAAATGAAAGTGAAGTGAAGTAGCCGGGCACGG	TGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCAAAGCGGGTGGATCACGAGGTCAG	GAGATCGAGACCATCCTGGCTAACATGGTGAAACCCCATCTCTAATAAAAATACAAAAAA	TTAGCTGGGCGTGGTGGCAGACGCCTGTAGTCCCAGCTACTCGGAAGGCTGAGGCAGGAGGCTGTHIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	AATGGCATGAACCCAGGAGGCAGAGCTTGCAGTGAGCCGAGTTTGCGCCCACTGCACTCCA	GCCTAGGTGACAGAGTGAGACTCCATCTCAAAAAAATAAAAATAAAAATAAAAATGAA 	AAAAAAAAGTGAAGTATAGAGTATCTCATAGTTTGTCAGTGATAGAACAGGTTTC	AAACTCAGTCATCTGACCGTTTGATACATCTCAGACACCACTACATTCAGTAGTTTAGA	TGCCTAGAATAAATAGAGAAGGAGAGATGGCTCTTCTCTTGTCTCATGGTTTCTTCTCTCTC	TGAGTGAGCTTGAATCACATGAAGGGAACAGCAGAAAACAACCAAC	TCATGTTTCCTTTAAAAGTCCCTGAAGGAAGGTCCTGGAATGTGACTCCCTTGCTCCTTT	GTTGCTCTTTTGGCATTCATTTCTTTGGACCCTACGCAAGGACTGTAATTGGTGGGGACGIIIIIIIIII	AGCTAGTGGCCCTGCTGGGCTTCACACGGTGTCCTCCCTAGGCCAGTGCCTCTGGAGT	CAGAACTCTGGTGGTATTTCCCTCAATGAAGTGGAGTAAGCTCTCTCATTTTGAGATGGT
3780	7841 3840	7901 3900	7961 3960	8021 4020	8081 4080	8141 4140	8201 4200	8261 4260	8321 4320	8381 4380	8441	8501 4500	8561 4560	8621 4620	8681 4680	8741 4740	8801 4800	8861
qq	Oy Dp	oy Dp	Qy Db	Qy Dp	Qy Dp	Qy Db	Qy Db	QY	Qy Dp	Qy Db	QY Dp	Qy Dp	Qy Dp	QY Db	QY Dp	QY Dp	Qy Db	δλ

9100 9160 5339 9400 9460 5459 9640 5159 cagaactctggtggtatttccctcaatgaagtggagtaagctctctcattttgagatggt 4919 Bovine butyrophilin; BT; human hereditary haemochromatosis; HFE; diagnosis; iron metabolism; NPT3; NPT4; RoRet; BTF1; BTF2; BTF3; BTF4; BTF5; milk protein; lupus; Sjogren's syndrome; hypophosphatemia; type 1 sodium transport gene; ss. Hereditary haemochromatosis subregion from an unaffected individual 5280 tcctgacctcgtgatccgcctgcctcggcctcccaaagtgctgaaattacaggtgtgagc 5460 ggtgcttcaggataccatatacagctcagaagtttcttcttttaggcattaaattttagca 5340 caccetgcccagccgtcaaaagagtcttaatatatatatccagatggcatgtgtttactt TCTCCTGTCTCAGCCTCCCAAGTAGCTGGGATTACAGGCGTGCACCACCATGCCCGGCTA CACCCTGCCCAGCCGTCAAAAGAGTCTTAATATATATATCCAGATGGCATGTGTTTACTT GGTGCTTCAGGATACCATATACAGCTCAGAAGTTTCTTCTTTAGGCATTAAATTTTAGCA GCTGTTATTTAATTAGCCAGTGAAAACTATTAACAACTTGTCTATTACCTGTTAGTATT ATAATGGAAGCCACCACCAAGTGGCTTAGAGGATGCCCAGGTCCTTCCATGGAGCCACTGGGG CTGGAGTGCAATGGCATGATCTCGGCTCACTGTAACCTCTGCCTCCCAGGTTCAAGCGAT TCCTGACCTCGTGATCCGCCTGCCTCGGCCTCCCAAAGTGCTGAGATTACAGGTGTGAGC TATGTTACTACATGCACTTGGCTGCATAAATGTGGTACAAGCATTCTGTCTTGAAGGGCA 9701 ATTGTTGCATTAAAAATGCATATACTTTAATAAATGTATATTGTATTGTA 9750 5700 attgttgcattaaaaatgcatatactttaataaatgtacattgtattgta 5749 RESULT 9
AAV57926/C
ID AAV57926 standard; DNA; 235033 BP.
XX
AC AAV57926;
XX
DT 23-DEC-1998 (first entry)
XX
DE Hereditary haemochromatosis subreg
XX
KW Bovine butyrophilin; BT; human her
KW diagnosis; iron metabolism; NPT3;
KW BTF4; BTF5; milk protein; lupus; KW
Type 1 sodium transport gene; ss. BP 5220 5400 9521 5520 5580 4860 8921 4980 9041 5040 9101 5100 9161 5160 9221 9281 9341 9401 9461 9581 9641 4920 8981 g οp g Ω g qq δy g δy qq ŏ QQ Qγ QQ δλ g οy οg δy Op δλ qq Qγ Qγ Qγ Qγ Qy δy

Thu Jun

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The present invention describes hereditary haemochromatosis gene products from the human haemochromatosis gene. The present sequence represents a hereditary haemochromatosis (HH). Also described is a method to determine the presence or absence of the common hereditary haemochromatosis (HH). Also described is a method to determine the presence or absence of the common hereditary haemochromatosis (HFE) gene mutation in an individual comprising:

CC (a) providing DNA or RNA from the individual; and (b) assessing the DNA or RNA for the presence or absence of the haplotype or genotype where the presence or absence of the haplotype genotype indicates the likely presence of the HFE gene mutation in the genome of the individual. The HFE gene sequences from the present invention can be used to develop products for use in the diagnosis and treatment of HFE. The present products for use in the diagnosis and treatment of HFE. The present invention also describes BFF genes, which are homologues of the milk and antagonists of BF function. Also described are: (1) a ROREt gene which can be used to develop products for the study, diagnosis and treatment of lugus and Sjogren's syndrome; and (2) NPT3 and NPT4 genes which are homologues of a type 1 sodium transport gene, and can
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Best Local Similarity 99.9%
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Db 42469 TGAGACGCACAGGTTTAATTTCTTTTCTCCATGCATATGGCTCAAGGGAA 42410 Oy 4741 GTGTCTAGGCCCTTGCTTTATTTAACCATAGCTTTTTTATATTTAATCTTTTTTAATCTTTTTAATCTTTTTAATTTAATAA	42409 GIGTCTATGCCCTTGCTTTTATTAACCAATAATCTTTGTATATTTATACCTGTTAA	4801 AAATTCAGAATGTCAAGGCCGGGCACGGTGGCTCACCCCTGTAATCCCAGCACTTTGGG [1] [1] [1] [1] [1] [1] [1] [1] [1] [1]	AGGCCGAGGCGGGTGGTCACAAGGTCAGGAGTTTGAGACCAGCCTGACCAACATGGTGAA [[[[[[[[[[[[[[[[[[[[[[[[[[[[[[[QY 4921 ACCCGTCTCTAAAAAATACAAAAATTAGCTGGTCACAGTCATGCGCACCTGTAGTCCCA 4980	QY 4981 GCTAATTGGAAGCCTGAGGCAGGAGCTTGAACCTGGAAGCGGAAGTTGCACTGA 5040	Oy 5041 GCCAAGATGGGGCCACTGCAGCTGGGGAGCAGGAGAGTCAATCTTAAAAA 5100	QY 5101 AAAAAAAAAAAAAAAGAATTCAGAGATCTCAGCTATCATATGAATACCAGGACAAA 5160	Qy 5161 ATATCAAGTGAGGCCACTTATCAGAGAACAATCCTTTAGGTTAAAAGTTTCTTCAT 5220	QY 5221 AGAACATAACAATAATCACTGAAGCTACCTATACAAGTCCGCTTCTTATAACAATGC 5280 (1100 110	QY 5281 CTCCTAGGTTGACCCAGGTGAAACTGACCATCTGTATTCAATGCACATAA 5340	QY 5341 AGGCCAATTTTATCTATCAGAACAAAGAACATGGGTAACAGATATGTATATTACATGTG 5400	Qy 5401 AGGAGAACAAGCTGATTGCTCTCCAAGTGACACTGTGTAAGAGTCCAATCTTAGG 5460	OY 5461 ACACAAATGGTGTCTCTCTGTAGCTTGTTTTTTCTGAAAAGGGTATTTCCTTCC	OY 5521 AACCTATAGAAGGAAGTGAAAGTTCCAGTCTTCCTGGCAAGGGTAAACAGATCCCTCTC 5580	Qy 5581 CTCATCCTCTTTCCTGTCAAGTGCCTCCTTTGGTGAAGGTGACACATCATGTGACC 5640	Qy 5641 TCTTCAGTGACCACTCTACGGTGTCGGGCCTTGAACTACTACCCCAGAACATCACCATG 5700	Qy 5701 AAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCTAAAGACGTATTG 5760	Qy 5761 CCCAATGGGGATGGACCTACCAGGGTGGATAACCTTGGCTGGTAAGGTG5820
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QQ	41389	CCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCCCTGGGGAAGAG	41330
Qy	5821	CAGAGATATACGTNCCAGGTGGAGCACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGG	5880 41270
O.Y	5881 41269	GGTATGTGACTGATGAGAGCCAGGAGCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCC	5940 41210
oy	5941	3GAGGTAATTATGGCAGTGAGATGAGGATCTGCTCTTTGTTAGGGGGTGGGCT	
Db	41209		
δδ	6001	GTGGCAATCAAAGGCTTTAACTTGTTTTTTAGAGCCCTCACCGTCTGGCACCCCCCCC	6060 41090
Oy	6061	TAGTCATTGGAGTCATCAGTGGAATTGCTGTTTTTGTCGTCATCTTGTTCATTGGAATTT	6120
Db	41089		41030
Oy	6121	TGTTCATAATATTAAGGAAGGGCAGGGTTCAAGTGAGTAGGAACAAGGGGGAAGTCTCT	6180
Db	41029		40970
Q7	6181	TAGTACCTCTGCCCCAGGCACAGTGGGAAGAGGGGCAGAGGGGATCTGGCATCCATGGG	6240
Op	40969		40910
Qy Db	6241	AAGCATITITCICATITATATICITIGGGACACCAGCAGCICCCCGGGAGACAGAAAIIIIIIII	6300 40850
Qy	6301	AATGGTTCTCCCCAGAATGAAAGTCTCTAATTCAACAAACA	6360
Db	40849		40790
ç	6361	TTTGCAAGAGCTGTTTAAGGTAGTACAGGGGCTTTGAGGTTGAGAAGTCACTGTGGCTAT	6420
G	40789		40730
Qy	6421	TCTCAGAACCCAAATCTGGTAGGGAATGAAATTGATAGCAAGTAAATGTAGTTAAAGAAG	6480
Db	40729		40670
λ	6481	ACCCCATGAGGTCCTAAAGCAGGAGGAAATGCTTAGGGTGTCAAAGGAAGAATG	6540
Q	40669		40610
Qy	6541	ATCACATTCAGCTGGGGATCAAGATAGCCTTCTGGATCTTGAAGGAGAAGCTGGATTCCA	6600
Dp	40609		40550
Qy	6601	TTAGGTGAGGTTGAAGATGATGGAGGTCTACACAGACGGAGCAACCATGCCAAGTAGGA [6660
Db	40549		40490
Qy Db	6661	GAGTATAAGGCATACTGGGAGATTAGAAATTACTGTACCTTAACCCTGAGTTTGCGT	6720 40430
Qy	6721	AGCTATCACTCACCAATTATGCATTTCTACCCCCTGAACATCTGTGGTGTAGGGAAAAGA	6780
Db	40429		40370
Qy	6781	GAATCAGAAAGAAGCCAGCTCATACAGAGTCCCAAGGGTCTTTGGGATATTGGGTTATGA	6840
Db	40369		40310
Qy	6841 40309	TCACTGGGGTGTCATTGAAGGATCCTAAGAAAGGAGGACCACGATCTCCCTTATATGGTG	6900 40250

2y 0b	6901 40249	AATGTGTTGTTAAGAAGTTAGATGAGAGGTGAGGAGACCAGTTAGAAAGCCAATAAGAT 6 	960
λ a	6961 40189	TTCCAGATGAGAGATAATGGTTCTTGAAATCCAATAGTGCCCAGGTCTAAATTGAGATGG 7. 	020
QQ Op	7021 40129	GTGAATGAGGAAAATAAGGAAGAGAGAGAGAGAGATGGTGCCTAGGTTGTGATGCCT 71	080
ζ ζ	7081	CTTICCTGGGTCTCTTGTCTCCACAGGAGCCATGGGGCACTACGTCTTAGCTGAACG 7:	140
ος O	7141	TGAGTGACACGCGGCTGCAGACTCACTGTGGGAAGACAAAACTAGAGACTCAAAGA 7:	200
2y Db	7201	GGGAGTGCATTTATGAGCTCTTCATGTTTCAGGAGAGAGTTGAACCTAAACATAGAAATT 7 	260
g Q	7261	GCCTGACGAACTCCTTGATTTTAGCCTTCTGTTCATTTCCTCAAAAAGATTTCCCCAT 7	320
ογ	7321	TTAGGTTTCTGAGTTCCTGCATGCCGGTGATCCCTAGCTGTGACCTCTCCCCTGGAACTG 7	7380 39770
QZ Dp	7381	TCTCTCATGAACCTCAAGCTGCATCTAGAGGCTTCCTTCATTTCCTCCGTCACCTCAGAG 7.	440
oy Db	7441 39709	ACATACACCTATGTCATTTCCTATTTTGGAAGAGGACTCCTTAAATTTGGGGGA 7	500
ογ	7501 39649	CTTACATGATTCATTTTAACATCTGAGAAAAGCTTTGAACCCTGGGACGTGGCTAGTCAT 7	'560 19590
λ G	7561 39589	AACCTTACCAGATTTTTACACATGTATCTATGCATTTTCTGGACCCGTTCAACTTTTCCT 7	620
Qy Db	7621 39529	TTGAATCCTCTCTCTGTGTTACCCAGTAACTCATCTGTCACCAAGCCTTGGGGATTCTTC 7	680
Qy Db	7681 39469	CATCTGATTGTGATGTGAGTTGCACAGCTATGAAGGCTGTACACTGCACGAATGGAAGAG 7	740
oy Oy	7741	GCACCTGTCCCAGAAAAGCATCATGGCTATCTGTGGGGTAGTATGATGGGTGTTTTTAGC 7	7800 39350
oy Oy	7801	AGGTAGGAGGCAAATATCTTGAAAGGGTTGTGAAGAGGTGTTTTTTCTAATTGGCATGA 7	19290
ργ	7861	AGGTGTCATACAGATTTGCAAAGTTTAATGGTGCCTTCATTTGGGATGCTACTCTAGTAT 7	920
QQ QA	7921 39229	TCCAGACCTGAAGAATCACAATAATTTTCTACCTGGTCTCTCCTTGTTCTGATAAATTTTCTACCTGGTCTCTCCTTGTTCTGATAAATTTTCTACCTGGTCTCTCCTTGTTCTGATAATTTTCTACCTGGTCTCTCCTTGTTCTGATAATGAAA 3	980

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804C 3911 810C 3905 3895	8220 3893 8280 3887	8340 3881 8400 3875	46 86 52	3863 8580 3857	8640 3851 8700	76	83	8880 3827	8940 3821	9000 3815	9060 3809	9120
ATTATGATAAGGATGATAAAAGCACTTACTTCGTGTCCGACTCTTCTGAGCACCTACTTA #############################	CACTTTGGGAGGCCAAAGCGGGTGGATCACGAGGTCAGGAGATCGAGACCCCATTTGGTTTTGGGAGGCCAAAGCGGGTGGATCACGAGGTCAGGAGATCGAGACCCAAAGCGGGTGGATCACGAGGTCAGGAGATCGAGACCCATCTCTAATAAAAATACAAAAAATTAGCTGGGGTTTTTTGGTGAAACCCCATCTCTAATAAAAATACAAAAAATTAGCTGGGCGTACATGATAAAAAATACAAAAAATTAGCTGGGCGTACATGATAAAAAATACAAAAAATTAGCTGGGCGTACATGATAAAAAATAAAAAAATAAGCTGGGCGGTACATGATAAAAAAATAAAAAAATAAGCTGGGCGGTACATGAAAAAAAA		CTCCATCTCAAAAAAATAAAAATAAAAATAAAAAAAAAA	AGAGTATCTCATAGTTTGTCAGTGATAGAAACAGGTTTCAAACTCAGTCAG	GAAGGAGATGGCTCTTCTCTTGTCTCATTGTGTTTCTTCTGAGTGAG	GANGGGAACAGCAACAACACAACTGATCCTCAGCTGTTGTTTGT	TTCTTTGGACCCTACGCAAGGACTGTAATTGGTGGGGACAGCTAGTGGCCCTGCTGGG	TTCACACACGGTGTCCTCAGGCCAGTGCCTCTGGAGTCAGAACTCTGGTGGTGTTTC	FA = FA	GCTTAGAGGATGCCCAGGTCCTTCCATGGAGCCACTGGGGTTCCGGTGCACTTAAAAA 	AAAATCTAACCAGGACATTCAGGAATTGCTAGATTCTGGGAAATCAGTTCACCATGTTCA 	AAAGAGTCTTTTTTTTTTTTGAGACTCTATTGCCCAGGCTGGAGTGCAATGGCATGAT '
7981 39169 8041 39109 8101	8161 38989 8221 38929	8281 38869 8341 38809	8401 8749 8461	38689 8521 38629	8581 38569 8641	70 70	876	8821 38329	8881 38269	8941 38209	9001 38149	9061
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37070 37670 37430 37250 10080 CCAGTCTTCACAGTAACACATTTCACTAACACATTTACTAAACATCAGCAACTGTGGCCT 10200 9420 9480 9540 9720 9780 9840 9240 9300 9360 0096 0996 0066 0966 AGTAGCTGGGATTACAGGCGTGCACCACCATGCCCGGCTAATTTTTGTATTTTAGTAGA GCTGCATAAATGTGGTACAAGCATTCTGTCTTGAAGGCCAGGTGCTTCAGGATACCATAT TATACTTTAATAAAATGTATATTGTATTGTATACTGCATGATTTTATTGAAGTTCTTGTTC AGGTAAGCATTTGTTTTATATTGGTTTTATTTCACCTGGGCTGAGATTTCAAGAAACACC AGAGTCTTAATATATATACCAGATGGCATGTGTTTACTTTATGTTAACTACATGCACTTG GCTGCATAAATGTGGTACAAGCATTCTGTCTTGAAGGGCAGGTGCTTCAGGATACCATAT ACGCTCATTGTAGAAAAGCTATAAAATGAATACAATTAAAGCTGTTATTTAATTAGCCAG TGAAAAACTATTAACAACTTGTCTATTACCTGTTAGTATTATTGTTGCATTAAAAATGCA CITTACATTTTGTCTTACGGAATATTTTCATTCAACTGTGGTAGCCGAATTAATCGTGT TCTTCACTCTAGGGACATTGTCGTCTAAGTTGTAAGACATTGGTTATTTTACCAGCAAAC CATTCTGAAAGCATATGACAAATTATTTCTCTCTTAATATCTTACTATACTGAAAGCAGA TGCCTCGGCCTCCCAAAGTGCTGAGATTACAGGTGTGAGCCACCCTGCCCAGCCGTCAAA ACAGCTCAGAAGTTTCTTCTTTAGGCATTAAATTTTAGCAAAGATATCTCATCTTCTT 9181 9241 9301 9361 9421 37729 9481 9541 37609 9601 9661 9721 9781 37369 9841 9901 9961 9121 37489 37249 10081 38089 38029 37969 37909 37849 37789 37669 37549 37429 37309 37189 10021 37129 37069 10141 Вþ δy qq qq QQ QQ g qq q QQ qq qq qq Q qq g QQ q g δλ Qy δ Qγ δy οy οy δ οy \dot{o} δy Óλ ò QY Qγ QΥ ōλ

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37009 CCAGTCTTCACAGTAACACTTTCACTAACACATTTACTAAACATCATCAGCAACTGTGGCCT 36950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HTV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaenia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                      CGCTGAGGGTTTTCCTGAAGGTAAAGGAATAAAGAATGGGTGGAGGGGGCGTGCACTGGAA
                                                                                                                                                                               ATCACTTGTAGAGAAAAGCCCCTGAAAATTTGAGAAAACAAAACAAGAAACTTACCTA
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                                                                               CATTTTAAATTCTTATTCACCTCTGGCAAAACCATTCACAAACCATGGTAGTAAAGAGAA
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                                                                                                                                                                             rising fragment of chemically modified gene, us treatment of diseases associated with abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 2115; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8622 BP; 2410 A; 100 C; 2013 G; 4099 T; 0 other;
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Qy Db	661 5522	CCCGGCTCTGCGGAGTGACTTTTGGAACCGCCCACTCCCCTTCCCCAACTAGAATGCTTT 720 	
Oy Dp	721 5582	TAAATAAATCTCGTAGTTCCTCACTTGAGCTGAGCTAGGGCCTGGGGCCTCCTTGAACCTGG 780 	
Oy Dp	781	AACTCGGGTTTATTCCAATGTCAGCTGTGCAGTTTTTTCCCCAGTCATCTCCAAACAGG 840 	
Qy Dp	841 5702	AAGTTCTTCCCTGAGTGCTTGCCGAGAAGGCTGAGCAAACCCACAGCAGGATCCGCACGG 900 	
Qy Dp	901 5762	GGTTTCCACTCAGAACGAATGCGTTGGGCGGGGGGCGCGAAAGAGTGGCGTTGGGGA 960 	
Qy	961	TCTGAATTCTTCACCATTCCACCCACTTTGGTGAGACCTGGGGTGGAGGTCTTAGGGT 1020 	
Oy Dp	1021 5882	GGGAGGCTCCTGAGAGGCCTACCTCGGGCCTTTCCCCACTCTTGGCAATTGTTCTTTT 1080 	
Qy Db	1081 5942	GCCTGGAAAATTAAGTAATATGTTAGATGTTTGAACTGAACTGAACAATTCTCTTTTCGG 1140 	
Oy Db	1141	CTAGGCTTTATTGATTTGCAATGTGCTGTGTAATTAAGAGGCCTCTCTACAAAGTACTGA 1200 	
Oy Dp	1201	TAATGAACATGTAAGCAATGCACTCCCACTTCTAAGTTACATTCATATCTGATCTTATTTGA 1260 	
Qy	1261 6122	TTTTCACTAGGCATAGGGAGGTAGCGCTAATAATACGTTTATTTTACTAGAAGTTAACT 1320 	
Oy Dp	1321	5-1	
Oy Db	1381	ATGTTATTTCAAGTACTACAGCTGCTTCTAATCTTAGTTGACAGTGATTTTGCCCTGTAG 1440 	
Oy Db	1441	TGTAGCACAGTGTTCTGTGGCTCACACGCCGCCTCAGCACACACTTTGAGTTTTGGTA 1500 	
Oy Dp	1501 6362	CGTGT# 	
Qy Db	1561 6422	CAAATTTATTCAATGGTACACTGGGCTTTGGTGGCAGAGCTCATGTCTCCCACTTCATAGC 1620 	
Oy Ob	1621 6482	TATGATTCTTAAACATCACACTGCATTAGAGGTTGAATAAAAATTTCATGTTGAGCAG 1680 	
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2640 6781 6901 2100 6961 2160 7021 7081 2280 2340 7201 2400 7261 2460 7321 2520 7381 2580 7441 7501 2700 7561 2760 AAACTTTGCCACATGTCACCTAGTAGACAACTCCTGGTTAAGAAGCTCGGGTTGAAAAA GCCACAAACAAGGTTGTGCAGGCGCTGTAGGCTGTGGTGTGAATTCTAGCCAAGGAGTA gttataaataaggttgtgtaggcgtttgtaggttgtggtggtgaattttagttaaggagta GTTCAAGACCAGCCTGGGCAACACAGCAAAACCCCCTTCTCTACAAAAATACAAAATTA GATGACAATAAGCAAATGAGCAGAAAGATATACAACATCAGGAAATCATGGGTGTTGTGA GAAGCAGAGAAGTCAGGGCAAGTCACTCTGGGGCTGACACTTGAGCAGAGAACATGAAGGA AATAAGAATGATATTGACTGGGAGCAGTATTTCCCAGGCAAACTGAGTGGGCCTGGCAAG CGGCGTGGGGGTGGGAAGGGGGACTACCATCTGCATGTAGGATGTCTAGCAGTATCCTGT CCTCCCTACTCACTAGGTGCTAGGAGCACTCCCCCAGTCTTGACAACCAAAAATGTCTCT AATAAACAAGTAGTGCTGGGGAGTAGAGGCCAAGAAGTAGGTAATGGGCTCAGAAGAGGA ACAGTGATCTGTCACAGGCTTTTAAAAGATTGCTCTGGCTGCTATGTGGAAAGCAGAATG AAGGGAGCAACAGTAAAAGCAGGGAGCCCAGCCAGGAAGCTGTTACACAGTCCAGGCAAG AGGTAGTGGAGTGGGTGGGAACAGAAAAGGGAGTGACAAACCATTGTCTCCTGAA TATATTCTGAAGGAAGTTGCTGAAGGATTCTÄTGTTGTGAGAGAAAGAAGAATTGG CTGGGTGTAGTAGCTCATGCCAAGGAGGAGGCCAAGGAGGAGCAGATTCCTGAGCACACGA GCTGGGTGTGGTGCATCCTGTGATCCTAGCTACTCGGGAGGCTGAGGTGGAGGGTA TTGCTTGAGCCCAGGAAGTTGAGGCTGCAGTGAGCCATGACTGTGCCACGTACTTCAGC CAAGGGAGAGAGCAGGGAAACAAGTCTTTACCCTTTGATATTTTGCATTCTAGTGGGAGA 6842 6962 7142 2341 6542 1741 6602 1801 6662 1861 6722 1921 6782 1981 2041 6902 2101 2161 7022 2221 7082 2281 7202 2401 7262 2461 7322 2521 7382 2581 7442 2641 7502 2701 7562 2761 7622 g Qγ QQ δλ QQ δy QQ δλ g οy QQ Óγ QQ Ω qq δy QΩ ΟŽ g δ g δy g δy qq Qγ Ω Ω QQ δ qq δy QQ òγ qq Qγ g

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                                    TGACTTTGTTCTTTATTTTAATTTTAGCCCTGAGCAGTGGGGTAATTGGCAATGCCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                     leic acid comprising fragment of chemically modified gene, us diagnosis and treatment of diseases associated with abnormal
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Pred. No. 0;
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Matches 2822; Conservative
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ōλ	421	
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Qy Db	481	GAAAAATCGAAACTTGTTTTTTTTTTGGGCTTTGGGAGTTTGGTAACTTTGGAGGACCTGC 540
οy	541	TCAACCCTATCCGCAAGCCCCTTCTCCCTACTTTCTGCGTCCAGACCCCGTGAGGGAGTGC 60
gg	3221	
λō	601	CTACCACTGAACTGCAGATAGGGGTCCCTCGCCCCAGGACCTGCCCCCTCCCCCGGCTGT 660
og .	3161	CTACCACTAAACTACAAATAAAAATCCCTCGCCCAAAACCTACCCCCTCCCCCGACTAT 3102
Oy Dp	661 3101	CCCGGCTCTGCGGAGTGACTTTTGGAACCGCCCACTCCCCTTCCCCCAACTAGAATGCTTT 720
ò á	721	TABATABATCTCGTAGTTCCTCACTTGAGCTGAGCTAGGGGCTCCTTGAACCTGG 780
an n	304 L	TAAATAAATCTCGTAATTCCTCACTTAAACTAAACTAAA
Qy	781	AACTCGGGTTTATTTCCAATGTCAGCTGTGCAGTTTTTTCCCCAGTCATCTCCAAACAGG 840
QY Db	841	AAGTICTICCCTGAGIGCTIGCCGAGAAGGCTGAGCAAACCCACAGAGGAICCGCACGG 900
δy	901	096
QQ	2861	AATTICCACTCAAAACGAATACGTTAAACGATAAAAACGCGAAAAAATAACGTTAAAAA 2802
Oy Dp	961	TCTGAATTCTTCACCATTCCACCCACTTTTGGTGAGACCTGGGGTGGAGGTCTCTAGGGT 1020
δλ	1021	GGGAGGCTCCTGAGAGGCCTACCTCGGGCCTTTCCCCACTCTTGGCAATTGTTCTTTT 1080
Q	2741	AAAAAACTCCTAAAAAAAAAAACCTACCTCGAACCTTTCCCCACTTTAACAATTTTTTTT
Oy Dp	1081	GCCTGGAAAATTAAGTATATGTTTTGAACGTTTGAACTGAACAATTCTCTTTTCGG 1140
QY	1141	CTAGGCTTTATTGATTTGCAATGTGCTGTGTAATTAAGAGGCCTCTCTACAAAGTACTGA 1200
ογ	1201	126
g G	2561	TAATAAACATATAAACAATACACTCACTTCTAAATTACATTCATATCTAATCTTATTTAA 2502
Qy Dp	1261	TTTCACTAGGCATAGGGAGGTAGGAGCTAATAATACGTTTATTTA
Qy Dp	1321	GGAATTCAGATTATATAACTCTTTTCAGGTTACAAAGAACATAAATAA
οy	1381	144
oqq	2381	ATATTATTICAAATACTACTACTICTAATCTTAATTAACATAATTTTACCCTATAA 2322

2142 1680 1800 2100 TGTAGCACAGTGTTCTGTGGGTCACGCCGGCCTCAGCACACACCACTTTGAGTTTTGGTA 1500 AATAAGAATGATATTGACTGGGAGCAGTATTTCCCAGGCAAACTGAGTGGGCCTGGCAAG 1980 AATAAAAATATATTAACTAAAAACAATATTTCCCAAACAAACTAAATAAACCTAACAAA 1782 2340 1482 2400 2460 CTACGTGTATCCACATTTTACACATGACAAGAATGAGGCATGGCACGGCCTGCTTCCTGG AAATATTCATTGTTTACAAGTGTAAATGAGTCCCAGCCATGTGTTGCACTGTTCAAGCCC CAAATTTATTCAATGGTACACTGGGCTTTGGTGGCAGAGCTCATGTCTCCACTTCATAGC CAAGGGAGAGCAGGGAAACAAGTCTTTACCCTTTGATATTTTGCATTCTAGTGGGAGA GATGACAATAAGCAAATGAGCAGAAAGATATACAACATCAGGAAATCATGGGTGTTGTGA CGGCGTGGGGGAAGGGGGACTACCATCTGCATGTAGGATGTCTAGCAGTATCCTGT AAACTTTGCCACATGTCACCTAGTAGACAAACTCCTGGTTAAGAAGCTCGGGTTGAAAAA GCCACAAACAAGGTTGTGCAGGCGCCTGTAGGCTGTGGTGTGAATTCTAGCCAAGGAGTA CCTCCCTACTCACTAGGTGCTAGGAGCACTCCCCCAGTCTTGACAACCAAAAATGTCTCT **ACAGTGATCTGTCACAGGCTTTTAAAAGATTGCTCTGGCTGCTATGTGGAAAGCAGAATG** AAGGGAGCAACAGTAAAAGCAGGGAGCCCAGGAAGCTGTTACACAGTCCAGGCAAG AGGTAGTGGAGTGGGCTGGGTAGCAAAAAGGGAGTGACAAACCATTGTCTCCTGAA 1441 2261 1561 2201 2081 1741 2021 1961 1841 1721 1501 1681 1981 2041 1661 1541 1801 1921 1781 2101 2161 1601 2221 2281 1481 2341 1421 2401 2461 1301 1361 g g óγ ò Qγ a g Ωp Db ò ολ Q οy qq Qλ g O. Do ò Db Óγ qq Qγ QQ Ω Q δ q Ω QQ δ qq δy QQ δ

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                                                                2941 TICTGAGATGGTGAAGGCAGAGAAAGAGCAGTTTGGGGTAAATCAAGGATCTGCATTTG 3000
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Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein;
43
                                                                                                                                                                                                                                                                                                                                            Human musculoskeletal system related polynucleotide SEQ ID NO 3113.
                                                 CCAGACACAGCTGATGGTATGATGCAGGTGTGTGGAGCCTCAACATCCTGCTCCC
                                                                     3721 CTCCTACTACACATGGTTAAGGCCTGTTGCTCTGTCTCCA 3760
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17-MAR-2000;
18-APR-2000;
19-MAY-2000;
07-JUN-2000;
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26-JUL-2000;
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The invention relates to novel genes (AAL34669-AAL37666) and proteins (ABB03087-ABB04109) associated with the musculoskeletal system useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune chycoiditis, diabetes mellitus, Crohn's disease, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, (c) cardiovascular discass such as myocardial isochemias; (d) wound parasitic infections diseases such as viral, bacterial, fungal and parasitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fip. infortuve diseases such as viral, bacterial.
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                              GAGACAGGGTTTCACCATGTTGGCCAGGCTGGTCTCGAACTCTCCTGACCTCGTGATCCG
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G93R"
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protein contains the mutation H63D"
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class I gene;
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"if this base is mutated to T, then protein contains the mutation S65C"
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"if this base is mutated to C,
protein contains the mutation
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The present sequence encodes a human histocompatibility iron loading (HFE) protein. The HFE gene is a major histocompatibility (MHC) mon-classical class I gene located on chromosome 6p. Mutations in the gene lead to iron disorders. The specification describes a method for disorder in a mammal. The method comprises determining the presence of a mutation in exon 2 or an introm of a HFE gene or protein. The mutation is not a C to G missense mutation at nucleotide 187 of the sequence juven in A96769 (Genbank Accession number U60319). The presence of the mutation indicates the disorder or the genetic susceptibility to the disorder. The method is used to diagnose an iron disorder e.g. haemochromatosis, or a genetic susceptibility to the e.g. haemochromatosis, or a genetic susceptibility to develop it.
                                                                                                                                                                                                                                                                                                                                                   Diagnosing an iron disorder e.g. hemochromatosis or a genetic susceptibility to develop it, by determining the presence of a mutation in exon 2 or an intron of a histocompatibility iron loading nucleic acid -
               f
"if this base is mutated to C, then the
protein contains the mutation I105T, which
is associated with an iron overload disorder"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7104 CAGGAGGACCATGGGGCACTACGTCTTAGCTGAACGTGACAGGCAGCCTGCAGAC
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98.7%; Pred. No. 1.8e-175;
iive 0; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2506 BP; 648 A; 552 C; 596 G; 710 T; 0 other;
                                                                                                                                                                                                                                                                        Barton JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 2-3; 55pp; English.
                                                                                                                                                                                                                                                                    Sawada-Hirai R,
                                                                                                                                                                  24-MAR-2000; 2000WO-US07982
                                                                                                                                                                                                   99US-0277457
                                                                                                                                                                                                                                   (BILL-) BILLUPS-ROTHENBERG
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Matches 1060; Conservative
 314
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P-PSDB; AAB19149.
                                                                                                                                                                                                                                                                  Rothenberg BE,
                                                                                                 WO200058515-A1
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(COUN-) COUNCIL QUEENSLAND INST MEDICAL RES
                BP
                                                                                          autosomal recessive disorder; ss.
               AAV23525 standard; mRNA; 2727
                                                                                                                                                          97WO-AU00539
                                                                                                                                                                         96AU-0002083.
                                                 (first entry)
                                                                 Haemochromatosis gene.
                                                                                                         Homo sapiens
                                                                                                                        WO9807884-A1
                                                                                                                                                         22-AUG-1997;
                                               10-JUL-1998
                                                                                                                                                                         03-SEP-1996;
23-AUG-1996;
                                                                                                                                         26-FEB-1998
                              AAV23525
       AAV23525
RESULT
                      CCGGTGATCCCTAGCTGTGACCTCTCCCCTGGAACTGTCTCTCATGAACCTCAAGCTGCA 7403
                                                                                                                                    rcctatititggaagactccttaaatttgggggacttacatgatttaacatc 7523
                                                                                                                                                             TCTAGAGGCTTCCTTCATTTCCTCCGTCACCTCAGAGACATACACCTATGTCATTTCATT
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TITAAIGGIGCCIICAIIIGGGAIGCIACICIAGIAIICCAGACCIGAAGAAICACAAIA 7943
                                                                                                                                                                                                                              Hereditary haemochromatosis; HC gene; HH identification; diagnosis;
                          tectatttttggaagaggaeteettaaatttgggggaettaeatgatteattttaaeate
                 TGAGAAAAGCTTTGAACCCTGGGACGTGGCTAGTCATAACCTTACCAGATTTTTACACAT
                                                CAGTAACTCATCTGTCACCAAGCCTTGGGGATTCTTCCATCTGATTGTGATGTGAGTTGC
                                                                                                                           ACAGCTATGAAGGCTGTACACTGCACGAATGGAAGAGGCACCTGTCCCAGAAAAAGCATC
                                                                                                                                                     ATGCCTATCTGTGGGTAGTATGATGGGTGTTTTTAGCAGGTAGGAGGCAAATATCTTGAA
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                                                                                                                This sequence represents the haemochromatosis (HC) gene. Mutations in this sequence are detected using the method of the invention. The method is for identifying an individual with hereditary haemochromatosis (HH) or a predisposition to develop HH or to genetically pass on HH to an offspring, comprising isolating a biological sample and amplifying a region of genomic DNA in the biological sample encompassing all or part of the DNA between markers D6226 and D62276, and detecting at least one homozygous or heterozygous mutation in a nucleoside within the region. The method can also be used for identifying an individual with an autosomal recessive disorder (ARD) or predisposition to develop and/or genetically pass on an ARD to an offspring, comprises isolating a biological sample from the individual and screening genomic DNA in the sample for the presence of a homozygous or heterozygous mutation in a cample for the method(s) can be used to identify individuals that are homozygous or heterozygous (carriers) for the mutation causing the ARD. Especially the method is used to diagnose HH or predisposition to the HB by detecting a Cys2827pr substitution. Individuals homozygous for this
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                                                          Detection of autosomal recessive disorder - particularly hereditary haemochromatosis, by detecting a mutation in the HC gene
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                                                                                                                                                                                                                                                                                                                                                                           Sequence 2727 BP; 702 A; 606 C; 660 G; 759 T; 0 other;
          Powell LW;
          BC,
           Jazwinska
                                                                                              Disclosure; Page -; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                             9.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
          Cullen LM,
                                  WPI; 1998-179064/16.
                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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Best Local Simi
Matches 1060;
          Busfield F,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New hereditary hemochromatosis gene products or polypeptides, useful for treating hereditary hemochromatosis in a patient, and as a metal chelation agent alleviating iron overload -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wolff
                  2065 attttctacctggtctctccttgttctgaaatgaaaattatgataaggatgataaagc
                                                                                                                                                                                                                                                                                                                                                                                                                                   CAGTAACTCATCTGTCACCAAGCCTTGGGGATTCTTCCATCTGATTGTGATGTGAGTTGC
                                                                                      TTTAATGGTGCCTTCATTTGGGATGCTACTCTAGTATTCCAGACCTGAAGAATCACAATA
                                                                                                                                                                                                                                                                                               7944 ATTTTCTACCTGGTCTCCTTGTTCTGATAATGAAATTATGATAAGGATGATAAAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TACAATAATTCTATGAGATAGGTACTATTATCCCCCATTTCTTTTAAATGAAGAAGTG
                                                                   ACAGCTATGAAGGCTGTACACTGCACGAATGGAAGAGGCACCTGTCCCAGAAAAAGCATC
                                                                                                                                     ATGGCTATCTGTGGGTAGTATGGGTGTTTTTAGCAGGTAGGAGGCAAATATCTTGAA
                                                                                                                                                                                                         AGGGGTTGTGAAGAGGTGTTTTTTTTTTAATTGGCATGAAGGTGTCATACAGATTTGCAAAG
                                                                                                                                                                                                                                                                                                                                                                                                              DNA used for mutation detection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human hereditary hemochromatosis
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96US-0632673.
96US-0652265.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BIRA ) BIO-RAD LAB INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drayna DT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-006341/01.
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16-APR-1996;
23-MAY-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-APR-1997;
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                                   The present invention relates to hereditary hemochromatosis gene products. These proteins may be used to treat a patient diagnosed as having human hemochromatosis disease. It is also useful as a metal chelation agent or as a T-cell differentiation factor, and for alleviating iron overload. They may also be used in protein replacement therapy for individuals having a defective human hemochromatosis gene.
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                                                                                                                                                                                                                          5507 TATTICCTICCTCCAACCTATAGAAGGAAGTGAAAGTTCCAGTCTTCCTGGCAAGGGTAA 5566
                                                                                                                                                                                                                                                                              ACAGATCCCCTCTCCTCTTCCTTTTCCTGTCAAGTGCCTCCTTTGGTGAAGGTGA 5626
                                                                                                                                                                                                                                                                                                                                  CACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTCGGGCCTTGAACTACTACTCCCCC 5686
                                                                                                                                                                                                                                                                                                                                                                                                                                       5747 CTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTAC 5806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTGAGAGGAGTGCCTGAGGGTAATTATGCCAGTGAGATGAGGATCTGCTCTTTGTTAG 5986
                                                                                                                                                                                                                                                                                           181 agaacatcaccatgaagtggctgaaggataagcagccaatggatgccaaggagttcgaac 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                          CCCCTGGGGAAGAGCAGAGATATACGTNCCAGGTGGAGCACCCAGGCCTGGATCAGCCCC
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                                                                                                                                                                                                  ;
0
                                                                                                                                                                        Length 517;
                                                                                                                                                                                                  1; Indels
                                                                                                                                 Sequence 517 BP; 126 A; 120 C; 147 G; 124 T; 0 other;
                                                                                                                                                                      Score 516; DB 22;
Pred. No. 1.5e-81;
0; Mismatches 1;
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            Disclosure; Fig 6; 108pp; English.
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                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 457)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project
                                                                                                                             (CGAP/BTGAP), Tumo
Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                           repetitive element ;, mRNA sequence. AI160732
Bonaldo, Ph.D
cDNA Library
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                                                                                                             Contact: Robert Strausberg, Ph.D.
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                                   cDNA Library Preparation: M. Bento Soares,
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                                                                                          cgapbs-r@mail.nih.gov
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by:
Greg
                                                                        N. Louis,
Lennon,
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Insert Length: 876 Std Error: 0.00
Seq.primer: -40ml3 fwd. ET from Amersham
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a 144 c 100 g 109 t
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/lab_host="DH10B"
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/clone_lib="NCI_CGAP_Brn23"
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/db_xref="taxon:9606"
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2752 TGGAGGGTATTGCTTGAGCCCAGGAAGTTGAGGCTGCAGTGAGCCATGACTGTGCCACTG
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Department of Eukaryotic Genomics
The Institute for Genomic Research
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CIT-HSP-2370L14.TR CIT-HSP Homo
                                                                                                                                                                                                                                                                                  http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: M13 Reverse
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                  Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1998)
Other_GSSs: CIT-HSP-2370L14.TF
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Adams, M.D., Rounsley, S.D.,
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AQ111002.1
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Use of a random human BAC
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Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and
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301 838 0200
301 838 0208
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                                                                                                                                                                                                /clone="2370L14"
/clone_lib="CIT-HSP"
                                                                                                                                                    /cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1:
                                                                                                                                                                                    /sex="Male"
                                                                                                                                                                                                                             /db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
Email: Cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D.,
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                               Tumor Gene Index Unpublished (1997)
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National Cancer Institute, Cancer Genome Ana
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/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from pooled breast tumor tissue, and was then primed with a Not I
                                                 /sex="female, pooled"
/tissue_type="breast"
/lab_host="DH10B"
                                                                                     /clone="IMAGE:1071428"
/clone_lib="NCI_CGAP_Br2"
/sex="female, pooled"
                                                                                                                                             /db_xref="taxon:9606"
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CTGTAATCCCAGCACTAAGGGAGCTGAGGCAGGTAGATCATTTGAGGTCAGGAGTGTGAG
                              CTGTAATCCCAGCACTTTGGTGGCCTGAGGCAGGTAGATCATTTGAGGTCAGGAGTTTGAG 3164
                                                                                                                                                                                                                            TAATTGGCAATGCCATTTCTGAGATGGTGAAGGCAGGAAAGAAGAGCAGTTTGGGGTAAAT 298
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                                                                                              GGCCACATAGGCAGTTCAGTGTAAGAATTCAGGACCAAGGCTGGGCACGGTGGCTCACTT 310
                                                                                                                              CAAGGATCTGCATTT-GGACATGTTAAGTTTGAGATTCCAGTCAGGCTTCCAAGTGGTGA 175
                                                                                                                                                                                             TAATTGGCAATGCCATTTCTGAGATGGTGAAGGCAGGGAAAGAGCAGTTTGGGGTAAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Mashington
401 Queen Anne Avenue North, Seattle, WA 98109,
Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: jwallace@u.washington.edu
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 2239 row: H column: 7
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1 (bases 1 to 533)

Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: !
    Location/Qualifiers
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Class: BAC ends
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E-Coli DH10B"
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/db_xref="taxon:9606"
/clone="plate=2239 Col=7 Row=H"
/clone_lib="CIT Approved Human
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Primates;
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Pred. No. 2.2e-48;
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Mammalia; Eutheria; I
1 (bases 1 to 525)
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similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christop
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence.
AW299376
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                                                                                                                                                                                                                                                                                                            153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            quality sequence stop: 464.
                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                           Fatima Bonaldo. "
123 c 125 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="NCI_CGAP_Kid11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="IMAGE:2771987"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'lab_host="DH10B"
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Pred. No. 2.9
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8787 TAATTGGTGGGGACAGCTAGTGGCCCTGCTGGGCTTCACACACGGTGTCCTCCCTAGGCC
                                                                                                                                                  8727 TCCCTTGCTCCTCTGTTGCTCTCTTTGGCATTCATTTCTTTGGACCCTACGCAAGGACTG
                                                                                                                                                                                                                                                                        TAATTGGTGGGGACAGCTAGTGGCCCTGCTGGGCTTCACACACGGTGTCCTCCCTAGGCC
                                                                                                                  TCCCTTGCTCCTCTTGCTCTTTGGCATTCATTTCTTTGGACCCTACGCAAGGACTG
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Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-GAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
National Cancer Institute, Cancer Genome Ana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1322376-1323911, 1456007-1456775, and 1500552-1502855). "Subtraction by Bento Soares and M. Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2771987 3' contains element MER37 repetitive element;, mRNA
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.9e-48;
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AW449998/c
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1 (bases 1 to 442)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                    The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LIAL at:

I.M.A.G.E. Consortium/LIAL at:

www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
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UI-H-BI3-aky-c-07-0-UI.sl NCI_CGAP_Sub5
                                                                                                                                                                                                                                                                                                                     Seq primer: M13 POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1997)
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     /Organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2735605"
/clone="IMAGE:2735605"
/clone="Iba=NCI_CGAP_Sub5"
/clone="DH10B (Life Technologies)"
/lab_host="DH10B (Life Technologies)"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT773D-Pac (Pharmacia) with a modified
/note="Vector: pT773D-Pac (Pharmacia) with a modified
/note="Vector: pT773D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; NCI_CGAP_Sub4. The
NCI_CGAP_Sub5 library had 3 million recombinants. A
single-stranded DNA preparation of NCI_CGAP_Sub4 was used
as a tracer in a subtractive hybridization with a driver
comprising: the IMAGE pool (NCI_CGAP_Kid3 pool 1 LIAM
334-3337, 3682-3683, 3798-3803 (IMAGE CloneIDs
1322376-1323911, 1450008-1456775,1500552-1502855);
NCI_CGAP_Kid5 pool 1 LIAM 338-3342,3727-3725, 3776-3778
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Best Local Similarity
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           sapiens genomic
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                                                AQ790990 533 bp DNA linear GSS 03-AU HS_2239_B1_D04_MR CIT Approved Human Genomic Sperm Library D sapiens genomic clone Plate=2239 Col=7 Row=H, DNA sequence.
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385 CTTCTCCTCCTGATGCTTTTGCAGACCGCGGTCCTGCAGGGGGCGCTTGCTGCTGAGTCC 444
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CCCTACTTTCTGCGTCCAGACCCCGTGAGGGAGTGCCTACCACTGAACTGCAGATAGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAGGGCTGCGGGCGAACTAGGGGCGCGGCGGGGGTGGAAAAATCGAAACTAGCTTTTTCT 504
                                                                                                                   TCCCTCGCCCCAGGACCTGCCCCCCCCCCGGCTGTCCCGGCTCTGCGGAGTGACTTTTG
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                                                                                                                                                 TCCCTCGCCCAGGACCTGCCCCCCCCCCGGCTGTCCCGGCTCTGCGGAGTGACTTTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Research 6, 791-806
TAG_LIB=NCI_CGAP_Co10
TAG_TISSUE=colon
TAG_SEQ=AAACG"
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                                9672 TAACAACTTGTCTATTACCTGTTAGTATTATTGTTGCATTAAAAATGCATATACTTTAAT 9731
                                                                                                                                                                                                                                                                                                                                                                                        403
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les 430; Conserv
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                                                                                                                                                    TCTTTTTTTGTGGTTAGAAAAGTTATGTAGAAAAAGTAAATGTGATTTACGCTCATTGT 164
                                                                                                                                                                          TCTTTTTTTGTGGTTAGAAAAGTTATGTAGAAAAAAGTAAATGTGATTTACGCTCATTGT 9611
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christop)
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Mashington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M. A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               National Cancer Institute, Cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 quality sequence stop: 406.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note-"Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; a modified polylinker; Site_1: Not I; Site_2: Eco RI; a modified polylinker; Site_1: Not I; Site_2: Eco RI; a modified polylinker; Site_1: Not I; Site_2: Eco RI; a modified plant of scircles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1323912-1328831, 1471368-1472903 and 1492104-1492555). Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fatima Bonaldo. "
84 c 82 g
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/clone_lib="NCI_CGAP_Kid12"
/tissue_type="2 pooled tumors (clear cell type)"
/lab_host="DH10B"
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/db_xref="taxon:9606"
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97.5%;
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RESULT
N93736/c
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                                                                                                                                                                       Query Match
Best Local :
                                                                                                                                           Matches
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                                                                                                                                           457;
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zb51g06.s1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:307162 3' similar to gb:M55053 CYTOCHROME P450 IA2 (HUMAN);
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Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: est@watson.wustl.edu
                                                                                                                                                                           Similarity
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/clone_lib="Soares_fetal_lung_NbHL19W"
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/db_xref="GDB:1250574"
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Pred. No. 1.2e-49;
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9349 CCAGCCGTCAAAAGAGTCTTAATATATATATCCAGATGGCATGTGTTTACTTTATGTTAC 9408

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ACCESSION
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AA876054/c
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ORGANISM
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similar to
                                                                                   Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Ilan Kirsch, M.D.,
                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Verte
Mammalia; Eutheria; Primates; Catarrhini; Hom
1 (bases 1 to 439)
NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
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                                                                                                                                                       Unpublished (1997)
                                                                                                                                                                              Tumor Gene Index
                                                                                                                                                                                                                                                                                                              Homo sapiens
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cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome
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Fatima Bonaldo. "
77 c 68 g
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                                                                                        Michael
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    Sequencing Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTTGTCTATTACCTGTTAGTATTATTGTTGCATTAAAAATGCATATACTTTAATAATGT 9737
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wq04f05.xl NCI_CGAP_Kid12 H
mRNA sequence.
AI949947
AI949947 GI:5742257
EST.
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Insert Length: 865 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham high quality sequence stop: 421.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modified polylinker; 1st strand cDNA was prepared from RER+ colon tumor, and was then primed with a Not I oligo(dT) primer. Double-stranded cDNA was ligated to Ec RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed bento Soares and M. Fatima Bonaldo (N-Soares4). "
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/db_xref="taxon:9606"
/clone="IMAGE:1161797"
/clone_lib="NCI_CGAP_Col0"
/tissue_type="colon tumor RER+"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab_host="DH10B"
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Pred. No. 2.3e-50;
                                                                              Homo
                                                                              sapiens cDNA clone
                                                                                             mRNA
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                                                                                             linear
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IMAGE: 2470305 3',
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Query Match
Best Local Similarity 99.7
Matches 432; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AI127651 438 bp mRNA linear EST 27-OC: qc30h07.xl Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clor iMAGE:1711165_3' similar to contains element MER36 repetitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           element ;, mRNA sequence.
AI127651
                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
TMASE Consortium (info@image.llnl.gov) for further information.

Insert Length: 669 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 415.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                         NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AI127651.1 GI:3596165
                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 438)
                                                                            153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           530
                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1711165"
/clone_lib="Soares_pregnant_uterus_NbHPU"
/sex="female"
                                                                                                                                                                                                                                                                                                  1. .438
                                                                                                                                                                                                       /lab_host-"DH10B"
                                                                                                                                                                                                                   /dev_stage="adult"
            4.0%;
99.1%;
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Score 429.6; DB Pred. No. 1e-50; Mismatches
  4;
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                         Length
                           438;
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                                                                                                                                                                                                                                                                    Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Seq
Clone distribution: NCI-CGAP clone distribution inf
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AW469921 440 bp mRNA linear EST 24-FEB-2000 ha27e08.x1 NCI_CGAP_Kidl2 Homo sapiens cDNA clone IMAGE:2874950 3' similar to contains Alu repetitive element;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                           quality sequence stop: 439.
Location/Qualifiers
/db_xref="taxon:9666"
/clone="ITMAGE:2874950"
/clone_lip="NCI_CGAP_Kidl2"
/tissue_type="2 pooled tumors (clear cell type)"
/lab_host="DHIOB"
/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not 1; Site_2: Eco RI;
plasmid DNA from the normalized library NCI_CGAP_Kid5 was
                                                                                                                                                                                   /organism="Homo sapiens"
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                                                                                                                                                                                                              .440
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Christopher Moskaluk, M.D., Ph.D.,
                                                                                                                                                                                                                                                                                                                                              Sequencing Center information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Michael R.
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                               GTTCAAAAGAGTCTTTTTTTTTTTTTTTGAGACTCTA 9091
                                                                                                                                            AAGTGGCTTAGAGGATGCCCAGGTCCTTCCATGGAGCCACTGGGGTTCCGGTGCACATTA 8995
                                                                                                                                                                                                           ATTTCCCTCAATGAAGTGGAGTAAGCTCTCTCTCATTTTGAGATGGTATAATGGAAGCCACC 8935
                                                             AAAAAAAAATCTAACCAGGACATTCAGGAATTGCTAGATTCTGGGAAATCAGTTCACCAT 65
                                                                                             AAAAAAAAATCTAACCAGGACATTCAGGAATTGCTAGATTCTGGGAAATCAGTTCACCAT 9055
                                                                                                                            AAGTGGCTTAGAGGATGCCCAGGTCCTTCCATGGAGCCACTGGGGTTCCGGTGCACATTA 125
                                                                                                                                                                                            ATTTCCCTCAATGAAGTGGAGTAAGCTCTCTCATTTTGAGATGGTATAATGGAAGCCACC
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Contact: John Quackenbush
The Institute for Genomic Research
The Institute for Genomic Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9712 Medical Center Dr.,
Tel: 301 838 3528
Fax: 301 838 0208
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Assessment of gene expression patterns in a model
metastasis using a 19,200 element cDNA microarray
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Hegde, P., Qi, R., Abernathy, K.,
, I.E., Saeed, A.I., Sharov, V.,
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Mammalia; Eutheria; Primates;
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330
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/db_xref="taxon:9606"
/clone_lib="MAGE resequences, MAGM"
/note="Vector: pBluescriptSKm"
137 c 123 g 132 t
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Pred. No. 1.1e-55;
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Lee,N.H., Y
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                                                                                               CAGCAGTTGCTGGAGCTGGGGAGAGGTGTTTTGGACCAACAAGGTATGGTGGAAACACAC
                                                                                                                                                                             CACAAGATTCGGGCCAGGCAGAACAGGGGCCTACCTGGAGAGGGACTGCCCTGCACAGCTG
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                     TTCTGCCCCTATACTCTAGTGGCAGAGTGGAGGAGGTTGCAGGGCACGGAATCCCTGGTT
                                                                                                                                                        CTCTTGATTCGGGCCAGGCAGAACAGGGCCTACCTGGAGAGGGACTGCCCTGCACAGCTG
                                                                            CAGCAGTTGCTGGAGCTGGGGAGAAGGTGTTTGGACCAACAAGGTATGGTGGAAACACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
plate: 1019 row: N column: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence-tagged connectors: A sequence approach to mapping scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
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GSS.
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Location/Qualifiers
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Class: BAC ends
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Keller,A., Shaker,R., Furlong,J.,
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Mammalia; Eutheria;
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Similarity 96.5%;
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                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen do and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"

114 c 146 g 137 t 5 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/dlone="plate=1019 Col=17 Row=N"
/clone_lib="RPCI-11 Human Male BAC Library"
/sex="male"
                                                                                                                                                                                                                                                                                                          0;
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0; Mismatches
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Pred. No. 1.3e-55;
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Young,J., Zhao,S.,
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AG116246
Pan troglodytes DNA, clone: PTB-123L15.R, genomic su AG116246
AG116246.1 GI:16736765
GSS; GSS (genome survey sequence).
Pan troglodytes male lymphoblast DNA, clone_lib:PTB
BAC Library clone:PTB-123L15.R.
                        2 (bases 1 to 648)
Fujiyama,A., Hattori,M., Toyoda,A.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                     Unpublished
                                                                                Totoki,Y., Watanabe,H. and Sakaki,Y. BAC end sequences of Library PTB
                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                      Pan
                Direct Submission
                                                                                                              Fujiyama,A.,
                                                                                                                            (sites)
                                                                                                                                                                     troglodytes
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(02-AUG-2001) Asao Fujiyama,
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98.9%;
                                                                                                             Hattori, M., Toyoda, A.,
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7;
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CTTTGAGTTTTGGTACTACGTGTATCCACATTTTACACATGACAAGAATGAGGCATGGCA 1545
                                                                                                                                                    GATTTIGCCCTGTAGTGTAGCACAGTGTTCTGTGGGTCACACGCCGGCCTCAGCACAGCA 1485
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                            CGGCCTGCTTCCTGGCAAATTTATTCAATGGTACACTGGGCTTTGGTGGCAGAGCTC 1602
                                                                CTTTGAGTTTTGGTACTACGTGTATCCACATTTTACACATGACAAGAATGAGGCATGGCA
                                                                                                                                  GATTTTGCCCTGTAGTGTAGCACAGTGTTCTGTGGGTCACACGCCGGCCTCAGCACAGCA 169
                                                                                                                                                                                                   TAATCTGGTTTTCTGATGTTATTTCAAGTACTACAGCTGCTTCTAATCTTAGTTGACAGT 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes/gsc.riken.go.jp/, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-911), Pax:81-45-53-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC enwas generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clone tracking errors.
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/clone_lib="PTB Chimpanzee Male
/clone_lib="PTB Chimpanzee Male
148 c 125 g 163 t
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/db_xref="taxon:9598"
/clone="PTB-123L15.R"
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AW974162

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mRNA

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02-JUN-2000

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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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1 TCTAAGGTTGAGATAAAATT......TCCCCAAATTTTTCATAAAC 10825
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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22 55																										
817 444	759	658	339	456	384	299	6146	650	612	822	308	292	420	326	318	445	334	368	388	441	540	448	393	454	385	380
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AL562711 B89781	AG185133	AG183592	AA102329	AQ483293	AI079088	R07647	AQ839831	AG116352	AQ395455	BG249643	AA319758	BF405650	AQ296898	AQ056874	BF446089	H01502	AW902003	BF739151	BF445847	R76697	AA088873	AI369750	AI763178	AI358948	AI760080	AI040303
AL562711 AL562711 B89781 CIT-HSP-217	w	AG183592 Pan trogl	AA102329 z190g03.r	AQ483293 RPCI-11-2	AI079088 oy51g10.s	R07647 ye98g01.s1	AQ839831 260L13-C4		AQ395455 CITBI-E1-	BG249643 602319736	AA319758 EST22021					H01502 yj21c03.s1	AW902003 QV0-NN102	BF739151 CM4-KT003	4	ч				AI358948 qy24g03.x	A1760080 wh62a10.x	AI040303 oy09c09.x

ALIGNMENTS

/lab_host="E.coli DH10 B" //ab_host="Re.coli DH10 B" //ab_host="Vector: pSPORT I; Site_1: SalI; Site_2: NotI; //ab_host="Re.coli DH10 B" //ab_host="Re.coli	BASE COUNT ORIGIN
1691 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_lib="HNC (Human Normal Cartilage)" /tissue tryoe="cartilage"	source
Fax: 610- Email: sa Seq prime	FEATURES
chKline eland R	
y Kumar	MEDLINE COMMENT
sequenced tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA libraries Osteoarthritis Cartilage 9 (7), 641-653 (2001)	JOURNAL
Sathe, G., Mui, P., Agarwal, P., Badger, A.M., Lee, J.C., Gowen, M. and Lark, M.W. Identification and initial characterization of 5000 expressed	TITLE
manmalia; Eutheria; Filmaces; Calairnin; nominitade; nomo. 1 (bases 1 to 691) Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,	REFERENCE AUTHORS
n. sapiens ryota; Metazoa; Chordata;	SOURCE
	ACCESSION VERSION
BG926549 691 bp mRNA linear EST 06-NOV-2001 HNC42-1-G8.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA	RESULT 1 BG926549/c LOCUS DEFINITION

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COMPUTER READABLE FORM:
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/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-652-265-7

US-08-834-497A-1

US-08-834-497A-7

US-08-834-497A-7

US-09-503-444A-1

US-09-503-444A-7

US-09-77-457-1

US-08-652-673B-3

US-08-652-673B-3

US-08-652-673B-13

US-08-652-673B-13

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US-08-834-497A-21
US-09-503-444A-20
US-09-503-444A-21
US-08-905-124-5
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Maximum Match 100%
Listing first 45 summaries
                                                     OM nucleic - nucleic search, using sw model
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Perfect score:
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LOCATION: join(361..436, 3762..4025, 4235..4510, 5606..5881, LOCATION: 6040..6153, 7107..7147)
OTHER INFORMATION: /product= "Hereditary Hemochromatosis OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER REALMANDLE 1978.

MEDIUM TYPE: FIDAPP disk
COMPUTER: IBM PC Compatible
GORPHATING SYSTEM: PC-DoS/MS-DOS
SOFTWARE: Patentin Release#1.0, Version #1.30
SOFTWARE: Patentin Release#1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: SALL, William M.
REPERANCE/DOCKET NUMBER: 17957-000500
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRHORE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                               APPLICANT: Thomas, Winston J.
APPLICANT: Thomas, Winston J.
APPLICANT: Drayna, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Ruddy, David
APPLICANT: Ruddy, David
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                       STREET: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California COUNTRY: USA ZIP: 94111-3834
Sequence 1, Application US/08652265 Patent No. 6025130 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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TYPE: nucleic acid
STRANDEDNESS: single
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Sequence Sequence ~

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genomic
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24d1(G)
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allele
/note= "No. 6025130mal or wild-type
Hereditary Hemochromatosis (HH) gene
allele"
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normal or wild-type (unaffected)
sequence surrounding variant for
allele (SEQ ID NO:20)"
                                                        /note= "start and stop positions
normal or wild-type (unaffected)
cDNA (SEQ ID NO:9)"
                                                                                                                /note= "start and stop positions
normal or wild-type (unaffected)
sequence surrounding variant for
allele (SEQ ID NO:41)"
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(unaffected)"
/label= 24d7
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(unaffected)"
/label= 24d1
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NAME/CET: allele
LOCATION: replace(5834, "g")
COTHER INFORMATION: /phenotype
OTHER INFORMATION: (unaffecte)
US-08-652-265-1
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NAME/KEY: allele
LOCATION: replace(3872, "c")
COTHER INFORMATION: (unaffect
OTHER INFORMATION: (label= 24)
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LOCATION: replace(3878, "a
OTHER INFORMATION: /phenot
OTHER INFORMATION: /label-
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LOCATION: 5507..6023
OTHER INFORMATION: 00
OTHER INFORMATION: SECONTER INFORMATION: SECONTER INFORMATION: SECONTER INFORMATION: 311
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                                         NAME/KEY: ...
LOCATION: 140..7319
OTHER INFORMATION: /
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LOCATION: 3852..3891
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           INFORMATION:
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ପ୍ଟମ	Qy	Qy	Qy Dp	Qy Db	Qy	Qy	oy og	Qy Dp	Q _Y	Oy Dp	Qy Dp	Qy Dp	Qy Dp	č d	Qy Dp	QY DP	Qy Dp	Qy

3540 2640 2640 2700 2700 2760 2760 2820 2820 2880 2880 2940 2940 3000 3000 3060 3060 3120 3120 3180 3180 3240 3240 3300 3300 3360 3360 3420 3420 3480 3480 3540 3600 3600 3660 TTGCTTGACCCCAGGAAGTTGAGGCTGCAGTGAGCCATGACTGTGCCACTGTACTTCAGC TCTAATTTGCCCTGAGCACCAACTCCTGAGTTCAACTACCATGGCTAGACACCCTTAAC GCTGGGTGTGGTGCATGCACCTGTGATCCTAGCTACTCGGGAGGCTGAGGTGGAGGGTA TGACTTTGTTCTTTATTTAATTTTATTGGCCTGAGCAGTGGGGTAATTGGCAATGCCAT TTCTGAGATGGTGAAGGCAGAGGAAAGAGCAGTTTGGGGTAAATCAAGGATCTGCATTTG CAGTGTAAGAATTCAGGACCAAGGCTGGGCACGGTGGCTCACTTCTGTAATCCCAGCACT TGGTGAAACCCCATGTCTACTAAAAATACAAAATTAGCCTGGTGTGGTGGCGCACGCCT ATAGTCCCAGGTTTTCAGGAGGCTTAGGTAGGAGAATCCCTTGAACCCAGGAGGTGCAGG CTCAAAAAAAAAAAAAAAAAAAAAAAAAAACTGAAGGAATTATTCCTCAGGATTTGGG **ACCCAGGACTGTCATATGGAAGAAAGACAGGACTGCAACTCACCTTCACAAAATGAGGA** GTTCAAGACCAGCCTGGGCAACACAGCAAAACCCCTTCTTACAAAAATACAAAAATTA CTAGGTGACAGAGCAAGACCCTGTCTCCCCTGACCCCCTGAAAAGAGAAGAGTTAAAGT GGACATGTTAAGTTTGAGATTCCAGTCAGGCTTCCAAGTGGTGAGGCCACATAGGCAGTT 2581 2641 2761 2821 2881 2941 2941 3001 3061 3181 3241 3241 3301 3301 3421 3421 3481 3541 3541 2581 2761 2821 3061 3121 3121 3181 3361 3361 3481 3601 3601 2701 2881 3001 2641 2701 qq g g qq g g δŽ Ω δy g δ Dβ QYqq Qy ΩD òγ g δy g ٥y g οy Ω QY ΩD Óγ d δ Ω δ ò Qγ ò οy

TCAACATCCTGGTCCC 3720 [[[390 396 396	ACAACCACAG 4020 CACACCACAG 4020 	CCTATTCCTT 4200	GTATGATGG 4320 ACCCAGGCC 4380 ACCCAGGCC 4380 ACCAGGCCTAC 4440 ACGGCCTAC 4440 ACGGCTAC 4460 ACGGCTAC 4500 AGGTCTTTG 4500 AGGTCTTTTG 4500 AGGTCTTTTG 4500	AGAGTGGAGG 4560
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3661 3661 3721 3721 3781 3781	841 841 901	3961 3961 4021 4081 4081	4141 4141 4201 4201 4261	4261 4321 4321 4381 4441 4441	4501 4501 4561 4621 4621 4681 4681
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4860 4980 5040 5040 5100 5100 5160 5160 5220 5220 5280 5340 5340 5400 5400 5460 5460 5520 5520 5580 5580 5640 5640 5700 5760 5760 5820 5880 5700 5820 5280 CAGAGATATACGTNCCAGGTGGAGCACCCAGGCTGGATCAGCCCCTCATTGTGATCTGG AAATTCAGAAATGTCAAGGCCGGGCACGGTGGCTCACCCCTGTAATCCCAGCACTTTGGG AGGCCGAGGCGGGTGGTCACAAGGTCAGGAGTTTGAGACCAGCCTGACCAACATGGTGAA GCTAATTGGAAGGCTGAGGCAGGAGCATCGCTTGAACCTGGGAAGCTGCACTGA GCCAAGATCGCGCCACTGCACTCCAGCCTAGGCAGCAGGAGTGAGACTCCATCTTAAAAAA AGAACATAGCAATAATCACTGAAGCTACCTATCTTACAAGTCCGCTTCTTATAACAATGC AGGGCAATTTTATCTATCAGAACAAGAACATGGGTAACAGATATGTATTTACATGTG AGGAGAACAAGCTGATCTGACTGCTCTCCAAGTGACACTGTGTTAGAGTCCAATCTTAGG TCTTCAGTGACCACTCTACGGTGTCGGGCCTTGAACTACTACCCCCAGAACATCACCATG AAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCTAAAGACGTATTG CCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCCCTGGGGAAGAG 5341 5401 4921 5041 5101 5101 5161 5221 5341 5521 5521 5581 4801 4861 4921 4981 5041 5161 5221 5281 5401 5641 5701 5701 5761 4741 4801 4861 4981 5281 5461 5461 5581 5641 5761 5821 Qy Db g Qγ Dp Ω g δý q οy g ò Ω ολ g οy Ω δ Ωp ò Op òγ QQ δy Ω δ g οy QQ Qγ Db δ Db δ g ò

AGATATACGTCCAGGTGGACCACC ATGTCACTGATCAGGAGCTG ATGTCACTGATCAGAGCCAGGAGCTG GGAGGTATTATGGCACGAGGCTG GGAGGTATTATGGCACTGAGATTACT TCATTGGATCACTGATCAGGAGTTGAGGGATCAGAGTTATTATAGGAGTCATTATTACTTAC	AGATATACGTCCAGGTGGACCACC ATGTCACTGATCAGGAGCTG ATGTCACTGATCAGAGCCAGGAGCTG GGAGGTATTATGGCACGAGGCTG GGAGGTATTATGGCACTGAGATTACT TCATTGGATCACTGATCAGGAGTTGAGGGATCAGAGTTATTATAGGAGTCATTATTACTTAC	GCCTGGATCAGCCCCTCATTGTGATCTGG 5880	AAAATCTATTGGGGGTTGAGAGGAGTGCC 5940 	TCTGCTCTTTGTTAGGGGGTGGGCTGAGG 6000	TGTTTTAGAGCCCTCACGGTCTGGCACCC 6060	TTTTGTCGTCATCTTGTTCATTGGAATTT 6120	AAGTGAGTAGGAACAAGGGGAAGTCTCT 6180 	AGGGCCAGAGGGATCTGCCATGGG 6240 	SGGACACCAGCAGCTCCCTGGGAGACAGAAAT 6300 	TCAACAACATCTTCAGAGCACCTACTAT 6360 	CTTTGAGGTTGAGAGTCACTGTGGCTAT 6420 	TTGATAGCAAGTAAATGTAAAGAAG 6480 	AAATGCTTAGGGTGTCAAAGGAAAGAATG 6540 	CTGGATCTTGAAGGAGAAGCTGGATTCCA 6600 	ICTACACAGACGAGCAACCATGCCAAGTAGGA 6660 	ATTACTGTACCTTAACCCTGAGTTTGCGT 6720 	CCCTGAACATCTGTGGTGTAGGGAAAAGA 6780 	CAAGGGTCTTTTGGGATATTGGGTTATGA 6840 	AGGAGGACCACGATCTCCCTTATATGGTG 6900 	TGAGGAGACCAGTTAGAAAGCCAATAAGCAT 6960
	5 8 8 8 5 5 8 8 8 8 5 8 8 8 8 8 8 8 8 8	AGAGATATACGTGCCAGGTGGAGCACCCAGGCC	GTATCTGACTGATGAGAGCCAGGAGCTGAC 	GAGGAGGTAATTATGGCAGTGAGAGATGAGGATCT 	SGCAATCAAAGGCTTTAACTTGCTTTTTCTGT 	agtcattggagtcatcagtggaattgctgttttt 	GTTCATAATATTAAGGAAGAGGCAGGGTTCAAGT 	AGTACCTCTGCCCCAGGG 	SCATTTTCTCATTTATATTCTTTG(SGTTCTCCCCAGAATGAAAGTCTCTAATT 	GCAAGAGCTGTTTAAGGTAGTACAGGGG 	CTCAGAACCCAAATC1 	CCCATGAGGTCCTAAAGCAGGCAGGAAGCAAGT 	ACATTCAGCTGGGATCAAGATAGCTT 	AGGTGAGGTTGAAGATGATGGGAGG 	GAGTATAAGGCATACTGGGAGATTAGAAATAATTACTGTAC 	GCTATCACTCACCAATTATGCATTTCTACCCCT 	AATCAGAAAGAAGCCAGCTCATACAGAGTCCAAG 	CACTGGGGTGTCATTGAAGGATCCTAAGAAAGGA 	AATGTGTTTAAGAAGTTAGATGAGAGGTGAGGA

7140 7140 7260 7320 7320 7380 7380 7440 7440 7500 7560 7560 7620 7680 7740 7740 7620 7800 7860 7920 7920 7980 8040 TICCAGATGAGATAATGGTTCTTGAAATCCAATAGTGCCCAGGTCTAAATTGAGATGG GTGAATGAGGAAAATAAGGAAGAAGAGAGAGAGACAAGATGGTGCCTAGGTTTGTGATGCCT TGAGTGACACGCAGCCTGCAGACTCACTGTGGGAAGGAGACAAAAACTAGAGACTCAAAGA GTGAATGAGGAAAATAAGGAAGAGAGAAGAGGCAAGATGGTGCCTAGGTTTGTGATGCCT CTTTCCTGGGTCTCTTGTCTCCACAGGAGGCCATGGGGGCACTACGTCTTAGCTGAACG GCCTGACGAACTCCTTGATTTTAGCCTTCTCTGTTCATTTCCTCAAAAAGATTTCCCCAT TTAGGTTTCTGAGTTCCTGCATGCCGGTGATCCCTAGCTGTGACCTCTCCCCTGGAACTG TCTCTCATGAACCTCAAGCTGCATCTAGAGGCTTCCTTCATTTCCTCCGTCACCTCAGAG ACATACACCTATGTCATTTCATTTCCTATTTTGGAAGAGGACTCCTTAAATTTGGGGGA TIGAATCCTCTCTCTGTGTTACCCAGTAACTCATCTGTCACCAAGCCTTGGGGATTCTTC CATCTGATTGTGATGTGAGTTGCACAGCTATGAAGGCTGTACACTGCACGAATGGAAGAG AGGTGTCATACAGATTTGCAAAGTTTAATGGTGCCTTCATTTGGGATGCTACTCTAGTAT TCCAGACCTGAAGAATCACAATAATTTTCTACCTGGTCTCTCCTTGTTCTGATAATGAAA 6961 7021 7081 7081 7141 7141 7201 7201 7261 7261 7321 7321 7381 7381 7441 7501 7561 6961 7021 7441 7501 7561 7741 7861 7621 7681 7681 7741 7801 7801 7861 7921 7921 7981 7981 Dp οy g δ g QΥ QQ QY q QΥ qq Qγ QQ οy OD δy Q Óγ g ÓΫ g Qγ Dp ΩŽ g οχ 엄 Ω Q ŏλ g qq a Qγ δ

Oy Dp	8041	CATGCATTACTGCATGCACTTCTTACAATAATTCTATGAGATAGGTACTATTATCCCCAT 8100
oy Dp	8101	TTCTTTTTAAATGAAAAAGAGAAGAGGCGGGCACGGTGGCTCACGCCTGTAATCCC 8160
Oy Dp	8161	AGCACTTTGGGAGGCCAAAGCGGGTGGATCACGAGGTCAGGATCGAGACCATCCTGGC 8220
O.y D.b	8221	TAACATGGTGAAACCCCATCTCTAATAAAAATACAAAAATTAGCTGGGGGTGGTGGCAG 8280
Oy Dp	8281	ACCCTGTAGTCCCAGCTACTCGGAAGGCTGAGGCAGGAGATGGCATGAACCCAGGAGG 8340
Qy Db	8341	CAGAGCTTGCAGTGAGCCGAGTTTGCGCCACTGCACTCCAGCCTGAGTGAG
Qy Db	8401	CTCCATCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
Oy Dp	8461 8461	TAGAGTATCTCATAGTTTGTCAGTGATAGAAACAGGTTTCAAACTCAGTCAATCTGACCG 8520
O Op	8521 8521	TTTGATACATCTCAGACACCACTACATTCAGTAGTTTAGATGCCTAGAATAAATA
Qy	8581 8581	GGAAGGAGATGGCTCTTCTCTTGTCTCTTTTTTTTGGGTGAGCTTGAATCACAT 8640
O.Y Db	8641	GAAGGGGAACAGCAGAAAACCAACTGATCCTCAGCTGTCATGTTTCCTTTAAAAGTC 8700
oy Dp	8701 8701	CCTGAAGGAAGGTCCTGGAATGTGACTCCCTTGTTGCTCTTTTTGGCATTCA 8760
Oy Db	8761 8761	TTTCTTTGGACCCTACGCAAGGACTGTAATTGGTGGGACAGCTAGTGGCCCTGCTGGGC 8820
Oy Dp	8821 8821	TTCACACGCGTGTCCTCCCTAGGCCAGTGCCTCTGGAGTCAGAACTCTGGTGGTATTTC 8880
Qy	8881 8881	CCTCAATGAAGTGGAGTAAGCTCTCTCATTTTGAGATGGTATAATGGAAGCCACCAAGTG 8940
Qy	8941	GCTTAGAGGATGCCCAGGTCCTTCCATGGAGCCACTGGGGTTCCGGTGCACATTAAAAAA 9000
Oy Dp	9001	AAAATCTAACCAGGACATTCAGGAATTGCTAGATTCTGGGAAATCAGTTCACCATGTTCA 9060
γ Oğ	90	AGAGTCTTTTTTTTTTTGAGACTCTATTGCCCAGGCTGGAGTGCAATGGCATGAT 912)
λ	93.21	CICGGCICACIGIAACCICIGCCICCCAGGIICAAGGATICICCIGICICAGCCICCCA 9180

Ωp	9121		18
QY	9181	GIAGCTGGGATTACAGGCGTGCACCACCATGCCCGGCTAATTTTTGTATTTTTAGTAGA 9	
QQ	9181	AGCTGGGATTACAGGCGTGCACCACCATGCCCGGCTAATTTTTGTATTTTTAGTAGA 9	Ö
QY	24	TGACCTCGTGATCCGCC 9	9300
q	9241	ACAGGGTTTCACCATGTTGGCCAGGCTGGTCTCGAACTCTCCTGACCTCGTGATCCGCC 9	(1)
οy	m i	TGCCTCGGCCTCCCAAAGTGCTGAGATTACAGGTGTGAGCCACCCTGCCCAGCCGTCAAA 9:	ε (
q d		GCCTCGGCCTCCCAAAGTGCTGAGATTACAGGTGTGAGCCACCCTGCCCAGCCGTCAAA	m
Qγ	36	AGAGTCTTAATATATATATCCAGATGGCATGTGTTTACTTTATGTTACTACATGCACTTG 9	₹
qq		GAGTCTTAATATATATCCAGATGGCATGTGTTTACTTTATGTTACTACATGCACTTG 9	4
Qy	9421	GCTGCATAAATGTGGTACAAGCATTCTGTCTTGAAGGGCAGGTGCTTCAGGATACCATAT 9	4
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Qy	9481	ACAGCICAGAAGITICITITAGGCAITAAAITITAGCAAAGATAICICATCITCIT 9	54
đ	9481	CAGCICAGAAGITICITITIAGGCATTAAATITITAGCAAAGATAICTCATCTICTT 9	54
Qy	54		9
Dp	9541	AAACCATTTTCTTTTTTGTGGTTAGAAAGTTATGTAGAAAAAAGTAAATGTGATTT 9	9
Qy	9601	ACGCTCATTGTAGAAAAGCTATAAAATGAATACAATTAAAGCTGTTATTTAATTAGCCAG 9	99
qa	9601	CGCTCATTGTAGAAAAGCTATAAAATGAATACAATTAAAGCTGTTATTAATTA	99
Óλ	9661	TGAAAAACTATTAACAACTTGTCTATTACCTGTTAGTATTATTGTTGCATTAAAAATGCA 9	9720
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Qγ	9721	TATACTTTAATAAATGTATATTGTATTGTATACTGCATGATTTTATTGAACTTCTTGTTC 9	78
qq	9721	ATACTTTAATAAATGTATTGTATTGTATACTGCATGATTTTATTGAAGTTCTTGTT	78
Oy d	7 1	ATCTTGTGTATATACTTAATCGCTTTGTCATTTTGGAGACATTTATTT	œ c
Q C	⊺8/6	TCTTGTGTATATATATATATATATATATATATATATATAT	4
Oy	9841	CTTTACATTTTGTCTTACGGAATATTTTCATTCAACTGTGGTAGCCGAATTAATCGTGTT 9	90
qq	9841	titacatitigicttacggaatattitcaticaactgiggtagcccaattaatcgigt	90
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QQ	9901	CTTCACTCTAGGGACATTGTCGTCTAAGTTGTAAGACATTGGTTATTTTACCAGCAAAC	96
Qy	9961	CATTCTGAAAGCATATGACAAATTATTTCTCTCTAAATATCTTACTAACTGAAAGCAGA 1	
qq	9961	ITCTGAAAGCATATGACAAATTATTTCTCTTTAATATCTTACTATACTGAAAGCAGA	10020
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QQ	10081	STAAGCATTTGTTTTATTTGGTTTTTTTTCACCTGGGCTGAGATTTCAAGAAACAC	014
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qa	10141	cagiciicacagiaacacaiiicaciaacacaiiiaciaaacaicagcaacigiggc	0
Qy	10201	GITAATITITIAATAGAAATITIAAGTCCTCATITICTITCGGTGTITITIAAGCTTA 1	10260

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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
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                                                                                                                                                                                                                  FEATURE
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                                                                                                       10321 CATTTTAAATTCTTATTCACCTCTGGCAAAACCATTCACAAACCATGGTAGTAAGAGAA 10380
                                                                                                                                                                    10681 TGAGAGGTACAGGCCAAAATTCTTATGTTGTATTATAATAATGTCATCTTATAATACTGT 10740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10741 CAGTATITIATATAAAACATICTICACAAACTCACACACATITAAAAAACAAAACACTGICTC 10800
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                                                                                                                                                  10381 GGGTGACACCTGGTGGCCATAGGTAAATGTACCACGGTGGTCCGGTGACCAGAGATGCAG
                                                                                                                                                                                                                 CGCTGAGGGTTTTCCTGAAGGTAAAGGAATAAAGAATGGGTGGAGGGGCGTGCACTGGAA
                                                                                                                                                                                                                                                                                                                                      10561 CTATTTGAATTGCTGGAATCACAGGCCATTGCTGAGCTGCCTGAACTGGGAACACAG
                                                                                                                                                                                                                                                                                                                                                                                                    AAGGAAAACAAACCACTCTGATAATCATTGAGTCAAGTACAGGAGGTGATTGAGGACTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/08652265

Sequence 3, Application US/08652265

Patent No. 6025130

GENERAL INPORMATION:
APPLICANT: Drayna, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Reddy, David
APPLICANT: Tsuchinashi, Zenta
APPLICANT: Tsuchinashi, Zenta
APPLICANT: Ruddy, David
APPLICANT: Ruddy, David
APPLICANT: Wolff, Roger K.
ITILE OF INVENTION: Hereditary Hemochromatosis G&
NUMBER OF SEQUENCES: 44

CORRESPENDENCE ADDRESS:
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STRATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0. Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10801 TAAAATCCCCAAATTTTTCATAAAC 10825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10801 TAAAATCCCCAAATTTTTCATAAAC 10825
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                             10261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 AATATCTAAAGTTCAGATCAGAACATTGCGAAGCTACTTTCCCCAATCAACAACACCCCT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TCTAAGGTTGAGATAAAATTTTTAAATGTATGATTGAATTTTGAAAATCATAAATATTTA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TCTAAGGTTGAGATAAAATTTTTAAATGTATGATTGAATTTTTGAAAATCATAAATATTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 10825;
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                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: join(361..436, 3762..4025, 4235..4510, 5606..5881, LOCATION: 6040..6153, 7107..7147)

OTHER INFORMATION: /product= "Hereditary Hemochromatosis OTHER INFORMATION: OTHER INFORMATION: mutation" OTHER INFORMATION: /note= "Hereditary Hemochromatosis OTHER INFORMATION: gene 24d1 allele" FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: replace(5834, "a")
COTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
OTHER INFORMATION:
COTHER INFORMATION: /label= 24dl
US-08-652-265-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAMALATION: 5507..6023
LOCATION: 5507..6023
OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: genomic sequence surrounding variant of the Rever Information: for 24d1(A) allele (SEQ ID NO:21)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 3852..3891
OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: genomic sequence surrounding variant OTHER INFORMATION: for 24d2(C) allele (SEQ ID NO:41)" PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: -
LOCATION: 140..7319
OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: 24d1 allele cDNA (SEQ ID NO:10)"
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100.0%; Pred. No. 0;
tive 0; Mismatches
                                                       17957-000500
                                 REGISTRATION NUMBER: 179
REFERENCE/DOCKET NUMBER: 179
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFRAX: (415) 576-0200
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 10825 base pairs
NAME: Smith, William M. REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3852..3891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 10823; Conser
                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: CDS
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TTTCCCCGCCCCCAAAAGAAG	:GGAGATTTAACGGGGACGTGCGCCAGAGCTGGGGAA 360 	GCTTCTCCTCTGATGCTTTTGCAGACCGCGGTCCTG 420	TGAGTCCGAGGGCTGCGGCGAACTAGGGCGCGGGGGGGGG	TTTGCGCTTGGGAGTTTGCTAACTTTGGAGGACCTGC 540 	TICCCTACTITCTGCGTCCAGACCCGTGAGGGAGTGC 600		TITGGAACCGCCACTCCCTTCCCCAACTAGAATGCTTT 720 	CACTIGAGCTGAGCTAAGCCTGGGGCTCCTTGAACCTGG 780 	CAGCTGTGCAGTTTTTTCCCCAGTCATCTCCAAACAGG 840 	CGAGAAGGCTGAGCAAACCCACAGGAGATCCGCACGG 900 	CGTTGGGCGGTGGGGGGCGCAAAGAGTGGCGTTGGGGA 960 	CCACTTTTGGTGAGACCTGGGGTGGAGGTCTCTAGGGT 1020 	CCTACCTCGGGCCTTTCCCCACTCTTGGCAATTGTTCTTTT 1080 	TAGTTTTGAACGTTTGAACTGAACAATTCTCTTTTCGG 1140 	GTGCTGTGTAATTAAGAGGCCTCTCTACAAAGTACTGA 1200 	CTCACTTCTAAGTTACATTCATATCTGATCTTATTTGA 1260 	raggagctaataatacgtttatttactagaagttaact 1320 	TTTCAGGTTACAAAGAACATAAATAATCTGGTTTTCTG 1380 	
2 2 2 2 2 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3	1 TTCCCCGCCCCCAAAAGAAGGGG 	1 ATGGCCCGCGAGCCAGGCCGGC	1 CAGGGCGCTTGCTGCG' 	1 GAAAAATCGAAACTAGCTTTTTCT 	1 TCAACCCTATCGCAAGCCCTCT	1 CTACCACT 1 CTACCACT	1 CCCGGCTCTGCGGAGTGACT	1 TAAATAAATCTCGTAGTTCCT 	1 AACTCGGGTTTATTTCCAATGT 	1 AAGTTCTTCCCTGAGTGCTTGC 	1 GGTTTCCACCTCAGAACGAATG 	TCTGAATTCTTCACCATTCCAC TCTGAATTCTTCACCATTCCAC	GGGAGGCTCCTGAGAGAGGC 	GCCTGGAAAATTAAGTATATGT 	1 CTAGGCTTTATTGATT	TAATGAACAT TAATGAACAT	TTTTCACTAGGCATAGGGAGG' TTTTCACTAGGCATAGGGAGG'	GGAATTCAGATTATATAACTCTT 	

2460 2520 2100 2280 2340 2340 2400 2400 2460 2040 2040 2100 2160 2160 2220 2220 2280 1920 1980 1440 1620 1620 1680 1740 1740 1800 1800 1860 AGGTAGTGGAGTGGGTGGGTGGGAACAGAAAGGGAGTGACAAACCATTGTCTGCTGAA ACAGTGATCTGTCACAGGCTTTTAAAAGATTGCTCTGGCTGCTATGTGGAAAGCAGAATG CGGCGTGGGGGTGGGAAGGGGGACTACCATCTCCATGTAGGATGTCTAGCAGTATCCTGT AATAAACAAGTAGTGCTGGGGAGTAGAGGCCAAGAAGTAGGTAATGGGCTCAGAAGAGGA GCCACAAACAAGGTTGTGCAGGCGCCTGTAGGCTGTGGTGAATTCTAGCCAAGGAGTA GAAGCAGAGAAGTCAGGGCAAGTCACTCTGGGGCTGACACTTGAGCAGAAGAAAGGA AATAAGAATGATATTGACTGGGAGCAGTATTTCCCAGGCAAACTGAGTGGCCTGGCAAG AAATATTCATTGTTTACAAGTGTAAATGAGTCCCAGCCATGTGTTGCACTGTTCAAGCCC CTACGTGTATCCACATTTTACACATGACAAGAATGAGGCATGGCACGGCCTGCTTCCTGG CAAATTTATTCAATGGTACACTGGGCTTTGGTGGCAGAGCTCATGTCTCCACTTCATAGC TGTAGCACAGTGTTCTGTGGGTCACACGCCGGCCTCAGCACACACTTTGAGTTTTGGTA 2401 2461 2041 2161 2221 2221 2281 2281 2341 2401 1921 1981 2041 2101 2101 2161 1861 1981 1441 1501 1621 1681 1681 1741 1741 1801 1801 1861 1921 1501 1561 1561 1621 1441 1381 P PP QY g δ g Db QΥ q ò QΥ q QCI δŽ g ōλ qq οy g Qγ qq δý QQ Q Dp οy Q pp òγ Óχ Op δ Óγ QΥ g

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	GCTGGGTGTGGTGCATCCTGTGATCCTACTACTGGGGGGGG	TTCTGAGATGGTGAAGGCAGAGGAAGGCAGTTTGGGGTAAATCAAGGATCTGCATTTG [[] [] [] [] [] [] [] [] [] [] [] [] []	TTGGTGGCTGAGGCAGGTAGATCATTGAGGTCAGGAGTTTGAGACAAGCTTGGCCAACA	TTGCAGTGAGCTGGAGTTGTGCCACTGCACCTGGGTGATAGAGTGAGCTGTGT	. ATTTCTAGAATCCACCAGCTTTAGTGGAGTCTGTCTAATCATGAGTATTGGAATAGGAT
4 10 10 10 10 10 14	2701 2761 2761 2821 2821 2881 2881	2941 2941 3001 3001 3061	3121 3121 3181 3181 3241	3301 3301 3361 3361 3421	3481 3481 3541 3541
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8 - 8 F	GIGICIAIGCCCTICCTITIATTIAACCAATAATCTITIGIAIATTATACCTGTTAA	AAATTCAGAAATGTCAAGGCCGGGCACGGTGGCTCACCCCTGTAATCCCAGCACTTTGGG	AGGCCGAGGCGGTGGTCACAAGGTCAGGAGTTTGAGACCAGCCTGACCAACATGGTGAA 	ACCGGCTCTAAAAAATACAAAAATTAGCTGGTCACAGTCATGCGCACCTGTAGTCCCA	GCTAATTGGAAGGCTGAGGAGGACCATCGCTTGAACCTGGGAAGCGGAAGTTGCACTGA 	GCCAAGATCGCGCCACTGCACTCCAGCCTAGGCAGCAGAGTGAGACTCCATCTTAAAAA 	aaaaaaaaaaaaaaaaagggaattcagggatctcagctatcatatgataccaggacaa 	ATATCAAGTGAGGCCACTTATCAGAGTAGAAGAATCCTTTAGGTTAAAGTTTCTTTC	AGAACATAGCAATAATCACTGAAGCTACCTATCTTACAAGTCCGCTTCTTATAACAATGC	CICCTAGGITGACCCAGGTGAAACTGACAICTGTAITCAATCAITTTCAATGCACATAA 	AGGGCAATTTTATCTATCAGAACAAGAACATGGGTAACAGATATGTATATTTACATGTG 	AGGAGAACAAGCTGATCTGACTGCTCTCCAAGTGACAGTGTTAGAGTCCAATCTTAGG 	ACACAAAATGGTGTCTCCTGTAGCTTGTTTTTTCTGAAAAGGGTATTTCCTTCC	AACCTATAGAAGGAAGTGAAAGTTCCAGTCTTCCTGGCAAGGGTAAACAGATCCCCTCTC	CTCATCCTTCTCTTTCTGTCAAGTGCCTCCTTTGGTGAAGTGACACATCATGTGACCTITICTTTTTTTTTT	TCTTCAGTGACCACTCTACGGTGTCGGCCTTGAACTACTACCCCCAGAACATCACCATG	AAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCTAAAGACGTATTG	CCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCCCTGGGGAAGAG
4681 4681 4741		4801	4861	4921	4981	5041	5101	5161	5221 5221	5281	5341	5401	5461	5521 5521	5581	5641	5701 5701	5761
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0069 5940 5940 0009 6000 0909 0909 6120 6120 6180 6180 6240 6240 6300 6300 6360 6360 6420 6420 6480 6480 6540 0099 0099 0999 0999 6720 6720 6780 6780 6840 TCACTGGGGTGTCATTGAAGGATCCTAAGAAAGGAGGACCACGATCTCCCTTATATGGTG AAGCATTTTTCTCATTTATATTCTTTGGGGACACCAGCAGCTCCCTGGGAGACAGAAAT TCTCAGAACCCAAATCTGGTAGGGAATGAAATTGATAGCAAGTAAATGTAGTTAAAGAAG ACCCCATGAGGTCCTAAAGCAGGCAGGAAGCAAATGCTTAGGGTGTCAAAGGAAAGAATG ACCCCATGAGGTCCTAAAGCAGGCAGGAAGCAAATGCTTAGGGTGTCAAAGGAAAGAATG CCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAG GGTATGTGACTGATGAGAGCCAGGAGCTGAGAAAATCTATTGGGGGGTTGAGAGGAGTGCC TGTTCATAATATTAAGGAAGAGGCAGGGTTCAAGTGAGTAGGAACAAGGGGGAAGTCTCT TTTGCAAGAGCTGTTTAAGGTAGTACAGGGGCTTTGAGGGTTGAGAAGTCACTGTGGCTAT ATCACATTCAGCTGGGGATCAAGATAGCCTTCTGGATCTTGAAGGAGAAGCTGGATTCCA TTAGGTGAGGTTGAAGATGATGGGAGGTCTACACAGACGGAGCAACCATGCCAAGTAGGA AGCTATCACTCACCAATTATGCATTTCTACCCCCTGAACATCTGTGGTGTAGGGAAAAGA GAATCAGAAAGAAGCCAGCTCATACAGAGTCCAAGGGTCTTTTGGGATATTGGGTTATGA CAGAGATATACGTNCCAGGTGGAGCACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGG GTGGCAATCAAAGGCTTTAACTTGCTTTTTCTGTTTTAGAGCCCTCACCGTCTGGCACCC TAGTCATTGGAGTCATCAGTGGAATTGCTGTTTTTTGTCGTCATCTTGTTCATTGGAATTT TAGTACCTCTGCCCCAGGGCACAGTGGGAAGAGGGGCAGAGGGGGATCTGGCATCCATGGG 5821 5881 5941 6001 6061 6121 6181 6241 6361 6421 6481 6481 6541 6541 5761 5821 5881 5941 6001 6061 6121 6181 6241 6301 6301 6361 6421 6601 6601 6661 6661 6721 6721 6781 6781 6841 ą g g λ 2γ q g ą g g q ą g ન ☆ ą ζ q λ $\frac{7}{2}$ ရ λ ą ~ ζ ζ ž ₹ ζ 3 ζ g ☆ ζ ζ ζ

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TCACTGGGGTGTCATTGAAGGATCCTAAGAAAGGAGGACCACGATCTCCCTTATATGGTG AATGTTGTTAAGAAGTTAGATGAGAGGTGAGGAGCCACGATCTCCCTTATATGGTG AATGTTGTTAAGAAGTTAAGAAGGAGGGGGAGACCAGTTAGAAAGCAT ATGTGTTGTTAAGAAGTTAAGAGGAGGGGGAGGAGGGTTAGAAAGCAT TTCCAGATGAGAGAATAATGGTTCTTGAAATCCAATAGTGCCCAGGTCTAAATTGAGATG TTCCAGATGAGGAAAATAAGGATTATGTTCTTGAAATCCAATAGTGCCCAGGTCTAAATTGAGAGG TTCCAGATGAGGAAAATAAGGAAGAGAGAGAGCCAAGATGGTGCCTAGGTTTGTGATGCCT GTGAATGAGGAAAATAAGGAAGAGAGAGAGCCAAGATGGTCCCTAGGTTTGTGATGCCT GTGAATGAGGAAAATAAGGAAGAGAGAGAGAGAGAGA	ATGACAGOTOLISTIC CONCACAGOGA AGGACA ACTAGOTOLISTANO ATGACA CGCAGCTGCAGACTCACTGGGGAAGGACACAAACTAGGCTAGAGATCAAGAGACTCAAAGAGACTCAAAGAACTAGAGACTCAAAGATTATAGACTTCACTGTGGGAAGGAA	STTICTEGGTTCCTGCATGCATCGTACCGTGGCCCTCTCCCCTGGAACT TCATGAACCTCAAGCTGCATCTAGAGGCTTCTTCATTTCCTCCGTCACCTCAGA TCATGAACCTCAAGCTGCATCTAGAGGCTTCTTTTTTTTT	TACCAGATTTTACACATGTATCTATGCATTTCTGGACCOGTTCAACTTTTCC [GCACCTGTCCCAGAAAAAGCATCATGGCTATTTTTTTTTT
6841 6901 6901 6961 7021 7021 7081	201 201 201 201 261 321	321 381 381 441 441 501	7561 7561 7621 7621 7681 7681	9 9 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8

Qy	7981	ATTATGATAAGGATGATAAAAGCACTTACTTCGTGTCCGACTCTTCTGAGCACCTACTTA 8040
Qy Db	8041	CATGCATTACTGCATGCACTTCTTACAATAATTCTATGAGATAGGTACTATTATCCCCAT 8100
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Qy Db	8161	AGCACTTTGGGAGGCCAAAGCGGGTGGATCACGAGGTCAGGAGTCGAGACCATCCTGGC 8220
QY	8221	TAACATGGTGAAACCCCATCTCTAATAAAAATACAAAAATTAGCTGGGCGTGGTGGCAG 8280
Qy	8281	ACGCCTGTAGTCCCAGCTACTCGGAAGGCTGAGGCAGGAGAATGGCATGAACCCAGGAGG 8340
Qy Up	8341	SAGCTIGCAGIGAGCCGAGTITGCGCCACIGCACTCCAGCCTAGGIGACAGAGIGAGA 8
QY	8401	CTCCATCTCRAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
Qy Db	8461	TAGAGTATCTCATAGTTTGTCAGTGATAGAAACAGGTTTCAAACTCAGTCAATCTGACCG 8520
Oy Ob	8521 8521	ထ ထ
Qy Db	8581 8581	GGAAGGAGATGGCTCTTCTCTTGTCTCATTGTGTTTCTTCTGAGTGAG
Qy	8641	GAAGGGGAACAGCAGAAAACAACCAACTGATCCTCAGCTGTCATGTTTCCTTTAAAAGTC 8700
Qy Dp	8701 8701	CCTGAAGGAAGGTCCTGGAATGTGACTCCCTTGTTCTTTTGGCATTCA 8760
Qy	8761 8761	TTTCTTTGGACCCTACGCAAGGACTGTAATTGGTGGGACAGCTAGTGGCCCTGCTGGGC 8820
Qy Db	8821	CACACACGGTGTCCTAGGCCAGTGCCTGTGGGGTTA
Qy Db	8881	CCTCAATGAAGTGGAGTAAGGTCTCTCATTTTGAGATGGTATAATGGAAGCCACCAAGTG 8940
Qy Db	8941	GCTTAGAGGATGCCCAGGTCCTTCCATGGAGCCACTGGGGTTCCGGTGCACATTAAAAA 9000
Oy Op	9001	AAAATCTAACCAGGACATTCAGGAATTGCTAGATTCTGGGAAATCAGTTCACCATGTTCA 9060

	10261	Oy 10381 GGGTGCACCTGGTGGCCATAG Db 10381 GGGTGACACCTGGTGGCCATAG Qy 10441 CGCTGAGGGTTTTCCTGAAGGT	10501 10501 10561 10561	Oy 10621 AGGAAACAAACCACTGAT Db 10621 AAGGAAAACAAACCACTCTGAT Oy 10681 TGAGAGGTACAGGCCAAAATTC Db 10681 TGAGAGGTACAGGCCAAAATTC Db 10681 TGAGAGGTACAGGCCAAAATTC	Oy 10741 CAGTATTTATAAAACATTCTT	RESULT 3 US-08-652-265-5 Sequence 5, Application US/086 Patent No. 6025130 GENERAL INFORMATION: APPLICANT: Thomas, Winston APPLICANT: Drayna, Dennis APPLICANT: Fedex, John N. APPLICANT: Girke, Andreas	APPLICANT: Ruddy, David APPLICANT: Tsuchihashi, Ze APPLICANT: Woulf, Woger K. TITLE OF INVENTION: Heredi NUMBER OF SEQUENCES: 44 CORRESPONDENCE ADDRESS: ADDRESSEE: Two Embarcadero STREET: Two Embarcadero CITY: San Francisco CITY: San Francisco COUNTRY: USA COUNTRY: USA COUNTRY: WEDIUM TYPE: Floppy disk MEDIUM TYPE: Floppy disk COMPUTER: READALE FORM: COMPUTER: TBM PC COMPATE
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8 6 6 6	8 6 8	0 <i>y</i> 0 <i>y</i> 0 <i>y</i>	6 6 6	9 9 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	6 6 6 6	6 6 6 6 6	

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ATTCTTAAGGTCAACTACATTTGAAAATCAAAGACCTG 10320
                                                                                      10440
                                                                                                                                CAGGCCATTGCTGAGCTGCCTGAACTGGGAACACAAAAG 10620
                                                                                                                                                                                                                               NTAATCATTGAGTCAAGTACAGCAGGTGATTGAGGACTGC 10680
                                                                                                                                                                                                                                                                                     CITAIGITGIAITAIAATAAIGICAICITAIAAIACIGI 10740
                                                                                                                                                                                                                                                                                             TITAAGICCICATITICITICGGIGITITITIAAGCITAA 10260
                                                                 GGTAAATGTACCACGGTGGTCCGGTGACCAGAGATGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ditary Hemochromatosis Gene
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o Center, Eighth Floor
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TAAAC 10825
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGCTGTAGGAGAGAGAACTAAAGTTCTGAAAGACCTGTTGCTTTTCACCAGGAAGTT
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                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
LOCATION: join(361..436, 3762..4025, 4235..4510, 5606..5881, LOCATION: join(361..436, 7107..7147)
LOCATION: 6040..6153, 7107..7147)
OTHER INFORMATION: /product= "Hereditary Hemochromatosis OTHER INFORMATION: mutation"
OTHER INFORMATION: /note= "Hereditary Hemochromatosis OTHER INFORMATION: /note= "Hereditary Hemochromatosis (HH) OTHER INFORMATION: gene 24d2 allele"
NAME/KEY: -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 10825;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ...carION: replace(3872, "g")

CTHER INFORMATION: /Phenotype= "Hereditary Hemochromatosis OTHER INFORMATION: /label= 2442

US-08-652-265-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: -
LOCATION: 5507..6023
OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: genomic sequence surrounding variant OTHER INFORMATION: for 24d1(G) allele (SEQ ID NO:20)" NAME/KEY: allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 3852..3891
OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: genomic sequence surrounding variant OTHER INFORMATION: for 24d2(G) allele (SEQ ID NO:42)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: 140..7319
OTHER INFORMATION: /note= "start and stop positions
OTHER INFORMATION: 24d2 allele cDNA (SEQ ID NO:11)"
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 10823; DB 3;
larity 100.0%; Pred. No. 0;
Conservative 0; Mismatches 2;
    #1.30
PatentIn Release #1.0, Version
                                                                                                                                                            17957-000500
                           APPLICATION NUMBER: US/08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William W. RGGISTRATION NUMBER: 17957-00050
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                          LENGTH: 10825 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                TYPE: nucleic
STRANDEDNESS:
TOPOLOGY: line
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Best Local Simil
Matches 10823;
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                                                                                                            ATGGGCCCGCGAGCCAGGCGGCGCTTCTCCTCCTGATGCTTTTGCAGACCGCGGTCCTG
                                                                          TTTCCCCGCCCCCCAAAAGAAGCGGAGATTTAACGGGGACGTGCGGCCAGAGCTGGGGAA
                                                                                                                                                                      TCAACCCTATCCGCAAGCCCCTCTCCCTACTTTCTGCGTCCAGACCCCGTGAGGGAGTGC
                                                                                                                                                                               CTACCACTGAACTGCAGATAGGGGTCCCTCGCCCCAGGACCTGCCCCCTCCCCCGGGCTGT
                                                                                                                                                                                                                 CCCGGCTCTGCGGAGTGACTTTTGGAACCGCCCACTCCCTTCCCCCAACTAGAATGCTTT
                                                                                                                                                                                                                                                 TAAATAAATCTCGTAGTTCCTCACTTGAGCTGAGCTAAGCCTGGGGCTCCTTGAACCTGG
                                                                                                                                                                                                                                                                                    781 AACTCGGGTTTATTTCCAATGTCAGCTGTGCAGTTTTTTCCCCAGTCATCTCCAAACAGG
                                                                                                                                                                                                                                                                                                                     AAGTTCTTCCCTGAGTGCTTGCCGAGAAGGCTGAGCAAACCCACAGGAGGATCCGCACGG
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1 GGAATTCAGATTATATAAACTCTTTTCAGGTTACAAAGAACATAAATAA	1 AIGTTATTICAAGTACTACAGCTGCTTCTAATCTTAGTTGACAGTGATTTTGCCCTGTAG 1440 	1 IGTAGCACAGTGTTCTGTGGGTCACACGCCGGCCTCAGCACACTTGAGTTTTGGTA 1500 	01 CTACGTGTATCCACATTTTACACATGACAAGAATGAGGCATGGCACGGCCTGCTTCCTGG 1560 	61 CAAATTTATTCAATGGTACACTGGGCTTTGGTGGCAGAGCTCATGTCTCCACTTCATAGC 1620 	21 TATGATTCTTAAACATCACACTGCATTAGAGGTTGAATAATAAAATTTCATGTTGAGCAG 1680 	1 AAATATTCATTGATTTACAAGTGTAAATGAGTCCCAGCCATGTGTTGCACTGTTCAAGCCC 1740 	1 CAAGGGAGAGGCAGGGAAACAAGTCTTTACCCTTTGATATTTTGCATTCTAGTGGGAGA 1800 	01 GATGACAATAAGCAAATGAGCAGAAAGATATACAACATCAGGAAATCATGGGTGTTGTGA 1860 	61 GAAGCAGAGAAGTCAGGGCAAGTCACTCTGGGGCTGACCTTGAGCAGAGACATGAAGGA 1920 	 21 AATAAGAATGATTGACTGGGGGGGGTATTTCCCAGGCAAACTGAGTGGGCCTGGCAAG 1980 21 AATAAGAATGATATTGACTGGGAGCAGTATTTCCCAGGCAAACTGAGTGGGCCTGGCAAG 1980 	81 TTGGATTAAAAAGCGGGTTTTCTCAGCACTACTCATGTGTGTG	11 CGGCGTGGGGGAAGGGGGACTACCATCTGCATGTAGGATGTCTAGCAGTATCCTGT 2100 	01 CCTCCCTACTCACTAGGTGCTAGGAGCACTCCCCCAGTCTTGACAACCAAAAATGTCTCT 2160 	61 AAACTTTGCCACATGTCACCTAGTAGACAAACTCCTGGTTAAGAAGGCTCGGGTTGAAAAA 2220 	221 AATAAACAAGTAGTGCTGGGGGTGTAGAGGCCAAGAAGTAGGTAATGGGCTCAGAAGAGGA 2280 	81 GCCACAAACAAGGTTGTGCAGCGCCTGTAGGCTGTGTGAATTCTAGCCAAGGAGTA 2340 	41 ACAGTGATCTGTCACAGGCTTTTAAAAGATTGCTCTGGCTGCTATGTGGAAAGCAGAATG 2400 	01 AAGGGAGCAACAGTAAAAGCAGGGAGCCCAGGAAGCTGTTACACAGTCCAGGCAAG 2460
132	138	144	15	15	16	y 168 b 168	y 174 b 174	18	18	19	Oy 196 Db 196	Qy 204 Db 204	Qy 210 Db 210	Qy 216 Db 216	Oy 222: Db 222:	Oy 226 Db 226	Oy 23, Db 23,	Oy 24(
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3300 3360 3420 3180 3180 3240 3240 3360 3420 3480 3480 ATTTCTAGAATCCACCAGCAGCTTTAGTGGAGTCTGTCTAATCATGAGTATTGGAATAGGAT 3540 2940 3000 3060 3060 3120 3120 2820 3000 2460 2520 2580 2640 2640 2700 2700 2760 2760 2820 2880 2880 CAGTGTAAGAATTCAGGACCAAGGCTGGCACGGTGGCTCACTTCTGTAATCCCAGCACT TTGCAGTGAGCTGAGATTGTGCCACTGCACTCCAGCCTGGGTGATAGAGTGAGACTCTGT GCTGGGTGTGGTGCATCCTGTGATCCTAGCTACTCGGGAGGCTGAGGTGGAGGTA TGACTTTGTTCTTTATTTTATTTGGCCTGAGCAGTGGGGTAATTGGCAATGCCAT TTCTGAGATGGTGAAGGCAGAGGGAAAGAGCAGTTTGGGGTAAATCAAGGATCTGCATTTG GGACATGTTAAGTTTGAGATTCCAGTCAGGCTTCCAAGTGGTGAGGCCACATAGGCAGTT ATAGTCCCAGGTTTTCAGGAGGCTTAGGTAGGAGAATCCCTTGAACCCAGGAGGTGCAGG GTTCAAGACCAGCCTGGGCAACACAGCAAAAACCCCTTCTACAAAAAATACAAAAATTA TTGCTTGAGCCCAGGAAGTTGAGGCTGCAGTGAGCCATGACTGTGCACTGTACTTCAGC **AGGTAGTGGAGTGGGCTGGGTAGGAAAAAGGGAGTGACAAACCATTGTCTCCTGAA** 3061 3181 3181 3241 3241 3301 3301 3361 3421 3421 3481 2941 2941 3001 3121 3121 3361 2881 3061 2401 2461 2521 2581 2581 2641 2641 2701 2761 2761 2821 2821 2881 3001 2461 2521 2701 g QΥ qq qq qq g g Ω Dp Db $^{\circ}$ g οχ g δy q ò 셤 ٥y Ω Ω g Qγ g οy Qγ δλ Ω δ g QQ QY δ Óλ g Ω

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ATTTCTAGAATCCACCAGCTTTAGTGGAGTCTGTCTAATCATGAGTATTGGAATAGGA CTGGGGGCAGTGAGGGGGGGGCAGCCACCTGTGGCAGAAAAGAG CTGGGGGCAGTGAGGGGGGGGCAGCCACCTGTGGCAGAAAAGAG CTGGGGGCAGTGAGGGGGGGGGGCAGCCACGTGTGGCAAAAAGCACAAAGGAAAAGAG ACCCAGGACTGTCATATGGAAGAAAAAGGCACTGCAACTCACCCTTCACAAATGAGG THILLIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHI	CTCCTACTACACATGGTTAAGGCCTGTTGCTCTCCAGGTTCACACTCTCTGCACTA CTCCTACTACACATGGTTAAGGCCTGTTGTTTTTTTTTT	TCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGCAGCTGAGTCTGAA	ATGCATCTTGAAGGAAACAGCTGGAAGTCTGAGGTCTTGTGGGAGGGA	GGCTGTGAAATGCAAGAAGAACAACGGGGGGGGTACTGGAAGTACGGGTATGATGGG [TGGCCCACCAACTGGAGTGGGAAAGGCACAAGATTCGGGCCAGGAGAACAGGCCTAC	GACCAACAAGGTATGGTGGAAACACACTTCTGCCCCTATACTCTAGTGGCAGAGGGGGGGG
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4920 5040 5100 5100 5160 5160 5220 5280 5340 5340 5400 5400 5460 5460 5520 5580 5700 GTGTCTATGGCCCTTGCTTTTATTTAACCAATAATCTTTTGTATATTATACCTGTTAA AAATTCAGAAATGTCAAGGCCGGGCACGGTGGCTCACCCCTGTAATCCCAGCACTTTGGG **AGGCCGAGGCGGGTGGTCACAAGGTCAGGAGTTTGAGACCAGCCTGACCAACATGGTGAA ACCCGTCTCTAAAAAAAATACAAAATTAGCTGGTCACAGTCATGCGCACCTGTAGTCCCA AAAAAAAAAAAAAAAAAAATTCAGAGATCTCAGCTATCATATGAATACCAGGACAAA** TCTTCAGTGACCACTCTACGGTGTCGGGCCTTGAACTACTACCCCCAGAACATCACCATG AGAACATAGCAATAATCACTGAAGCTACCTATCTTACAAGTCCGCTTCTTATAACAATGC AGGGCAATTTTATCTATCAGAACAAGAACATGGGTAACAGATATGTATTTACATGTG AGGAGAACAAGCTGATCTGACTGCTCTCCAAGTGACACTGTGTTAGAGTCCAATCTTAGG ACACAAAATGGTGTCTCTCTGTAGCTTGTTTTTTTCTGAAAAGGGTATTTCCTCCTCC CTCATCCTTCCTCTTTCCTGTCAAGTGCCTCCTTTGGTGAAGGTGACATCATGTGACC 4741 4621 4741 5041 5041 4621 4681 4681 4801 4801 4861 4861 4921 4921 4981 4981 5101 5101 5161 5161 5221 5281 5341 5341 5221 5281 5401 5461 5461 5641 5641 5401 5521 5521 5581 5581 g αq qq δλ ۵y g qq Qγ Óγ Qγ g QQ q οý δ ò δý g QΫ́ g οy g δ Q QΥ οq Qγ D δy g Qγ g δy Ω οy qq

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AAGTGGCTGAAGGATAAGCACCCAATGGATGCCAAGGAGTTCGAACCTAAAGACGTATTG AAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCTAAAGACGTATTG AAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCTAAAGACGTATTG CCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAG CCCAATGGGGATGGACCTACCAGGCTGGATAACCTTGGCTGTACCCCTGGGGAAGAG CAGAGATATACGTGCCAGGCTGGATAACCTTGGCTGTACCCCTGGGGAAGAG CAGAGATATACGTGCCAGCCCCAGGCTGGATCACCCCTCATTGTGATCTGG CATAGTGATGAGAGCCAGGACCAGACCTGGATCAGCCCCTCATTGTGTTTTTTTT	GAGGAGGTAATTATGGCAGTGAGATGAGGATCTGCTCTTTGTTAGGG GAGGAGGTAATTATGGCAGTGAGATGAGGATCTGCTCTTTGTTAGGG TGGCAATCAAGGCTTTAACTTGCTTTTTCTGTTTTAGAGCCTCAC	TCATAATATTAAGGAAGAGGCAGGGTTCAAGTGAG 	AAGCATTTTCTCATTTATATTCTTTGGGACACCAGCAGCTCCCTGGGAGACAAAT	TGCAAGAGCTGTTTAAGGTAGTACAGGGCCTTTGAGGTTGAGAAGTCACTGTGGCTTA'	ACCCCATGAGGTCCTAAAGCAGGCAGGAAATGCTTAGGGTGTCAAAGGAAAGAATG	AGGTGAGGTTGAAGATGATGGGAGGTCTACACAGACGGGGGAACCATGCCAAGTAGGTAG
5701 <i>b</i> 5701 <i>b</i> 5701 <i>b</i> 5701 <i>b</i> 5761 <i>c</i> 5821 <i>c</i> 5821 <i>c</i> 5881 <i>c</i> 5881 <i>c</i> 5881	941 941 001 001 061		6241 6241 6301 6301	4 4 3 6 2 4 2 6 2	6481 6481 6541 6541 6601	6601 6661 6661 6721 6721 6781
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7680 7680 7800 7560 7560 7620 0069 7020 7020 7080 7080 7140 7140 7200 7260 7320 7320 7380 7440 7440 7500 AGGIGICATACAGATTIGCAAAGTITAATGGTGCCTTCATTIGGGATGCTACTCTAGTAT GCCTGACGAACTCCTTGATTTTAGCCTTCTCTGTTCATTTCCTCAAAAAGATTTCCCCAT AACCITACCAGATTITIACACATGTATCTATGCATTTTCTGGACCCGTTCAACTTTTCCT TTGAATCCTCTCTCTGTGTTACCCAGTAACTCATCTGTCACCAAGCCTTGGGGATTCTTC CATCTGATTGTGATGTGAGTTGCACAGCTATGAAGGCTGTACACTGCACGAATGGAAGAG GCACCTGTCCCAGAAAAGCATCATGGCTATCTGTGGGTAGTATGATGGGTGTTTTTAGC CITICCTGGGICTCTTGTCTCCACAGGAGGAGCCATGGGGCCACTACGTCTTAGCTGAACG TIAGGITICIGAGITCCTGCATGCCGGTGATCCCTAGCTGTGACCTCTCCCCTGGAACTG TCTCTCATGAACCTCAAGCTGCATCTAGAGGCTTCCTTCATTTCCTCCGTCACAGAG ACATACACCTATGTCATTTCATTTCCTATTTTGGAAGAGGACTCCTTAAATTTGGGGGA TGAGTGACACGCAGCCTGCAGACTCACTGTGGGAAGGAGACAAAACTAGAGACTCAAAGA GTGAATGAGGAAAATAAGGAAGAGAGAAGAGGCAAGATGGTGCCTAGGTTTGTGATGCCT 7621 7681 7741 7741 7801 7801 7441 7561 7621 7681 7021 7081 7081 7141 7141 7201 7201 7261 7321 7321 7381 7381 7441 7501 7501 7561 7861 6781 6841 6841 6901 6901 6961 6961 7021 7261 Op qq g δλ q οy qq οy g Qγ qq Ω g δ g QY οq δy g ŏ g δŽ g ò QQ g Óλ δy g δ g δy Ω g οy δ

qq	7861	AGGTGTCATACAGATTTGCAAAGTTTAATGGTGCCTTCATTTGGGATGCTACTCTAGTAT 7920		
0	7921	CCTGAAGAATCACAADAATTTTCTACCTGGTCTCTCCTTGTTCTGATAATGAA 798	Qy	9001 AAAATCT
e e	7921	- ō	qa	
φy	7981	ATTATGATAAGGATGATAAAAGCACTTACTTCGTGTCCCGACTCTTCTGAGCACCCTACTTA 8040	oy 1	9061 AAAGAGTC
QQ	7981	ATTATGATAAGGATGATAAAAGCACTTACTTCGTGTCCGACTCTTCTGAGCACCTACTTA 8040	2 2	
VO do	8041	CATGCATTACTGCATCCACTTCTFACAATAATTCTATGAGATAGGTACTATTATCCCCAT 8100	qq	9121 CTCGGCTC
δý	8101	TTCTTTTTAAATGAAGAAGTGAAGTAGGCCGGGCACGGTGGCTCACGCCTGTAATCCC 81	Qy Dp	9181 AGTAGCT(9181 AGTAGCT(
qq	8101	TTCTTTTTAAATGAAGAAAGTGAAGTAGGCCGGGCACGGTGGCTCACGCCTGTAATCCC 816	δλ	9241 GACAGGG
δ S S	8161	AGCACTTTGGGAGGCCAAACGGGTGGATCACGAGGTCAGGAGTTCAAGACCATCCTGGC 8220 	, qa	-0
δy	8221	TAACATGGTGAAACCCCATCTCTAATAAAAATACAAAAATTAGCTGGGCGTGGTGGCGG 82	Q <u>y</u>	9301 TGCCTCGC
අ	8221	TAACATGGTGAAACCCCATCTCTAATAAAATACAAAAATTAGCTGGGCGTGGTGGCGG 828	QY	9361 AGAGTCT
δ δ	8281	ACGCCTGTAGTCCCAGCTACTCGGAAGGCTGAGGCAGGAGAATGGCATGAACCCAGGAGG 8340 	qa	 9361 AGAGTCT
3 6	8341	NGGCC101RGICCCRGCIRCICGGRANGGCIGARGGCRGGRANGGCRIGARCCCRGGRAGG 504 CAGAGCHTGCRGTGAGCCGAGTTTGCGCGCACTGCACTCCAGAGTGAAGATGAAA	QY	9421 GCTGCAT
7 d	8341	CAGAGCTTGCAGTGAGCCGAGTTTGCGCCACTCCAGCCTAGGTGACAGAGCGAGA 840	qq	9421 GCTGCATA
0γ.	8401	CTCCATCTCRAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	δλ	9481 ACAGCTC2
Dp	8401	CTCCATCTCAAAAAAATAAAAATAAAAAATAAAAAATGAAAAAAAA	g :	9481 ACAGCTO
γο 42 42	8461	TAGAGTATCTCATAGTTTGTCAGTGATAGAAACAGGTTTCAAACTCAGTCAATCTGACCG 8520 	d d	9541 TTAAACC
3 8	8531	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	ΟŊ	9601 ACGCTCAS
g 4	8521	TITGATACAILLAGAGACACCACTACATACATACATACATACATACATACAT	qa	9601 ACGCTCA
Qy	8581	GGAAGGAGGGGGTCTTCTCTTGTCTCATTGTGTTTCTTCTGAGTGAG	ζ, Q	9661 TGAAAAA(9661 TGAAAAA
g	8581	98	Oy	
λ c	8641	GAAGGGGAACAGCAGAAAACAACCAACTGATCCTCAGCTGTCATGTTTCCTTTAAAAGTC 8700 	qq	TATACT
3 8	8701	CCTGAAGGAAGGAAGGAAAGGAAAGGAAAGGAAAGGAAA	QY	9781 ATCTTGT
7 g	8701	CCTGAAGGAAGGTCCTGGAATGTGACTCCCTTGTTTTTTTT	QQ	781
Qy	8761	TITCTIIGGACCCIACGCAAGGACIGIAAIIGGIGGGGACAGCIAGIGGCCCIGCIGGGC 882	ර් සි	9841 CTTTACA 9841 CTTTACA
q	8761	TITCITIGGACCCTACGCAAGGACT	δ	L
Qy d	8821	TICACACACGGTGTCCTCCCTAGGCCAGTGCCTCTGGAGTCAGAACTCTGGTGGTATTIC 8880 []	ad d	9901 TCTTCAC
3 3	9 0	700 0001747400450190177754450471504501771775754547777561547477777777777777777	δŏ	9961 CATICIG
g g	8881	CUITARIANGENEGARIANGENTULARIANGENTARIANGENTARIANGENGENTARIANGENGENTE 8940 CUITARIANGENGENGENGENGENTETTIGRAGATGGANGCAACAAGTG 8940 CUITARIANGENGENGENGENGENGENGENTARIANGENAGCAACAAGTG 8940	qa	
δλ δ	94	GCTTAGAGGATGCCCCAGGTCCTTCCATGGAGCCACTGGGGTTCCGGTGCACATTAAAAA 9	do do	10021 CTGCTATA 10021 CTGCTATA
Q C	894 I			

CTCTAGGGACATTGTCGTCTAAGTTGTAAGACATTGGTTATTTTACCAGCAAAC ITAATAAATGTATATTGTATTGTATACTGCATGATTTTATTGAAGTTCTTGTTC SINTCACCATGITGGCCAGGCTGGTCTCGAACTCTCCTGACCTCGTGATCCGCC TTAATATATATATCCAGATGGCATGTGTTTACTTTATGTTACTACATGCACTTG CATTITITITITITITGEGTTAGAAAGTTATGTAGAAAAAAGTAAATGTGATTIT ACTATTAACAACTTGTCTATTACCTGTTAGTATTATTGTTGCATTAAAAATGCA ATTITICICITACGGAATATTITCATTCAACTGTGGTAGCCGAATTAATCGTGTT PAACCAGGACATTCAGGAATTGCTAGATTCTGGGAAATCAGTTCACCATGTTCA |CTTTTTTTTTTTTTTGAGACTCTATTGCCCAGGCTGGAGTGCAATGGCATGAT regeattacagecetecaccaccateccegectaatttttattagtaga

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FEATURE:
NAME/KEY: allele
LOCATION: replace(3872, "g")
OTHER INFORMATION: /Phenotype= "Hereditary Hemochromatosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /phenotype= "Hereditary Hemochromatosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "start and stop positions for genomic sequence surrounding variant for 24d1(A) allele (SEQ ID NO:21)"
ZIP: 94111-3834

COMPUTER REAABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION: 514
ATYORNEY/AGENT INFORMATION:
NAME: SMITH, William M.
NAME: SMITH, William M.
NAME: SMITH, William M.
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 576-0200
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 10025 base pairs
TYPE: nucleic acid
STRANDENESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 3;
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11arity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
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LOCATION: replace(5834, "a")
COTHER INFORMATION: /phenotype
OTHER INFORMATION: /label= 24
US-08-652-265-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic)
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OTHER INFORMATION:
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Best Local Similarity
Matches 10823; Conser
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Sequence 7, Application US/08652265

Sequence 7, Application US/08652265

Patent No. 6025130

GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
APPLICANT: Drayna, Dennis T.
APPLICANT: Girke, Andreas
APPLICANT: Girke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Ruddy, David
APPLICANT: WOLIf, Roger K.
TITLE OF INVENTION: Hereditary Her
NUMBER OF SEQUENCES: 44

CORRESPONDENCE ADBRESS:
CORRESPONDE
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	aatatctaaagttcagatcagaacattgcgaagct 	TCAGGATTTAAAACCAAGGGGACACTGGATCAC 	CTGCTGTAGGAGAGAGACTAAAGTTCTGAAAGAC 	TTACTGGGCATCTCCTGAGCCTAGGCAATAGCTGT/ 	TTTCCCCCCCCCCAAAAGAAGGGGAGATTTAACG 	ATGGCCCGCGAGCCAGCCGGGCTTCTCCTCCTCTCTCTCT	CAGGGCCTTGCTGCGTGAGTCCGAGGCTGCGG 	GAAAATGGAAACTAGCTTTTTGTTTGCCTTGGG 	TCAACCCTATCGCAAGCCCTCTCCCTACTTTCTC 	CTACCACTGAACTGCAGATAGGGGTCCCTCGCCCC 	CCCGGCTCTGCGGAGTGACTTTTGGAACCGCCCAC	TAAATAAATCTCGTAGTTCCTCACTTGAGCTGAGC 	AACTCGGGTTTATTTCCAATGTCAGCTGTGCAGTT 	aagticticctgagtgcttgccgagaaggctgagg 	GGTTTCCACCTCAGAACGAATGCGTTGGGCGGTGC 	TCTGAATTCTTCACCATTCCACCCACTTTTGGTGA(GGGAGGCTCCTGAGAGGCCTACCTCGGGCCTTT 	GCCTGGAAAATTAAGTATATGTTAGTTTTGAACGTTT
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2040 2040 2100 2160 1920 1980 1980 2100 2160 1260 1440 1440 1500 1560 1620 1620 1680 1680 1740 1740 1800 1800 1860 1860 1920 1140 1200 1320 1320 1380 1380 1500 1560 GCCTGGAAAATTAAGTATATGTTAGTTTTGAACGTTTGAACTGAACAATTCTCTTTTCGG TAATGAACATGTAAGCAATGCACTCACTTCTAAGTTACATTCATATCTGATGTTATTGA ATGTTATTTCAAGTACTACAGCTGCTTCTAATCTTAGTTGACAGTGATTTTGCCCTGTAG ATGTTATTTCAAGTACTACAGCTGCTTCTAATCTTAGTTGACAGTGATTTTGCCCTGTAG TGTAGCACAGTGTTCTGTGGGTCACACGCCGGCCTCAGCACACCACTTTGAGTTTTGGTA CTACGTGTATCCACATTTTACACATGACAAGAATGAGGCATGGCACGGCCTGCTTCCTGG TATGATTCTTAAACATCACACTGCATTAGAGGTTGAATAATAAAATTTCATGTTGAGCAG AAATATTCATTGTTTACAAGTGTAAATGAGTCCCAGCCATGTGTTGCACTGTTCAAGCCC GATGACAATAAGCAAATGAGCAGAAAGATATACAACATCAGGAAATCATGGGTGTTGTGA GAAGCAGAGAAGTCAGGGCAAGTCACTCTGGGGCTGACACTTGAGCAGAGACATGAAGGA CGGCGTGGGGGAAGGGGGGACTACCATCTGCATGTAGGATGTCTAGCAGTATCCTGT TAATGAACATGTAAGCAATGCACTCACTTCTAAGTTACATTCATATCTGATGTTATTTGA CTAGGCTTTATTGATTTGCAATGTGCTGTGTAATTAAGAGGCCTCTCTACAAAGTACTGA TTTTCACTAGGCATAGGGAGGTAGGAGCTAATAATACGTTTATTTTACTAGAAGTTAACT 1741 1981 1081 1141 1141 1201 1201 1261 1261 1321 1321 1381 1381 1441 1441 1501 1501 1561 1561 1621 1681 1681 1741 1801 1801 1861 1921 1921 1981 2041 2101 2101 1621 Dp q Db g g qq g δ q QΫ g δy Dp Qγ QQ Qγ Dp QΥ Db άy pp ρp Dp g Qγ q οy οy δλ QY Ω ΟŊ QY Ω QY QΥ

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4320 4380 4380 3900 4140 4140 4200 4200 4260 4260 4320 4440 3840 3840 3900 3960 3960 4020 4020 4080 4080 3720 3720 3780 3780 3360 3420 3480 3480 3540 3600 3600 3660 4381 TGGCCCACCAAGCTGGAGTGGGAAAGGCACAAGATTCGGGCCAGGCCAGAACAGGGCCTAC GGCTGTGAAAATGCAAGAAGACAACAGTACCGAGGGCTACTGGAAGTACGGGTATGATGGG ATGCATCTTGAAGGAAACAGCTGGAAGTCTGAGGTCTTGTGGGAGCAGGGAAGAGGGAAG GAATTIGCTICCIGAGAICATITGGICCTIGGGGAIGGIGGAAAIAGGGACCIAIICCII CAGGACCACCTTGAATTCTGCCCTGACACTGGATTGGAGAGCAGCAGAACCCAGGGCC CCTCTTCATGGGTGCCTCAGGAGCAGGACCTTGGTTTCTTTTGAAGCTTTGGGCTA CGTGGATGACCAGCTGTTCGTGTTCTATGATNATGAGAGTCGCCGTGTGGAGCCCCGAAC AGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTATGGAAAATCACAACCAAG CAAGGGTATGTGGAGAGGGGGCCTCACCTTCCTGAGGTTGTCAGAGCTTTTCATCTTTTC **ACCCAGGACTGTCATATGGAAGAAGACAGGACTGCAACTCACCCTTCACAAAATGAGGA** CTGGGGGCAGTGAGGGGTGGCACCACGTGTGGCAGAGAAAAGACACACAAGGAAAGAGC TTGCAGTGAGCTGAGATTGTGCCACTGCACTCCAGCCTGGGTGATAGAGTGAGACTCTGT CTCAAAAAAAAAAAAAAAAAAAAAAAAAAAACTGAAGGAATTATTCCTCAGGATTTGGG 4321 4261 4321 3961 4021 4081 4141 4141 3781 3841 3901 3901 3961 4021 4081 3781 3841 3481 3541 3541 3601 3601 3661 3661 3721 3721 3301 3301 3361 3361 3421 3421 3481 g ò g Qγ В QΥ ρp ò Q 8 Qy Db g g g Dp q οy qq ٥y QQ QY Q οy P QΥ QQ Ω Ω QΥ Ω Ω Qγ qq οy δ

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Qy	4441	CTGGAGAGGGACTGCCCTGCACAGCTGCAGAGTTGCTGGAGCTGGGGAGAGGTGTTTTG 4500 	
oy Db	4501	GACCAACAAGGTAIGGIGGAAACACACTICIGCCCCTAIACICTAGIGGGAAGIGGAGG 4560 	
Qy Db	4561	AGGTTGCAGGGCACGGAATCCCTGGTTGGAGTTTCAGAGGTGGCTGAGGCTGTGTGCCTC 4620	
QY	4621	TCCAAATTCTGGGAAGGGACTTTCTCAATCCTAGAGTCTCTACCTTATAATTGAGATGTA 4680 	
Qy Db	4681	TGAGACAGCCACAAGTCATGGGTTTAATTTCTTTCTCCATGCATATGGCTCAAAGGAA 4740 	
Qy Db	4741	GTGTCTATGGCCCTTG 	
Qy	4801	AAATTCAGAAATGTCAAGGCCGGGCACGGTGGCTCACCCCGTAATCCCAGCACTTTGGG 4860 	
QY	4861	AGGCCGAGCCGGTCACAAGGTCAGGAGTTTGAGACCAGCCTGACCAACATGGTGAA 4920	
Qy	4921	ACCCGTCTCTAAAAAATACAAAAATTAGCTGGTCACAGTCATGCGCACCTGTAGTCCCA 4980 	
Qy Dp	4981	GCTAATTGGAAGGCTGAGGAGCATCGCTTGAACCTGGGAAGCGGAAGTTGCACTGA 5040 	
Qy Db	5041	GCCAAGATCGCGCCACTGCACTCCAGCCTAGGCAGCAGAGGCTGCATCTTAAAAAA 5100 	
Qy Dp	5101 5101	aaaaaaaaaaaaaaaaagaattcagagatctcagctatcatgaataccaggacaaa 5160 	
Qy Dp	5161 5161	ATATCAAGTGAGGCCACTTATCAGAGTAGAAGAATCCTTTAGGTTAAAAGTTTCTTTC	
Qy Db	5221 5221	AGAACATAGCAATAATCACTGAAGCTACCTATCTTACAAGTCCGCTTCTTATAACAATGC 5280 	
Qy Dp	5281 5281	CTCCTAGGTTGACCCAGGTGAACTGACCATCTGTATTCAATCATTTTCAATGCACATAA 5340 	
QY	5341	AGGGCAATTTTATCTATCAGAACAAGAACATGGGTAACAGATATGTATATTTACATGTG 5400 	
Qy Db	5401	AGGAGAACAAGCTGATCTGACTGCTCTCCAAGTGACACTGTGTTAGAGTCCAATCTTAGG 5460 	
οy	5461	AAAAGGTATTCCTTCCTCC 552	

5940 6240 5580 5640 5700 5700 5760 5760 5820 5820 5880 5940 0009 0009 0909 6120 6180 6180 6240 6300 6300 6360 6360 6420 6420 6480 6480 6540 6540 0099 0099 AACCTATAGAAGGAAGTGAAAGTTCCAGTCTTCCTGGCAAGGGTAAACAGATCCCCTCTC CTCATCCTTCCTCTTTCCTGTCAAGTGCCTTCTTTGGTGAAGGTGACATCATGTGACC TCTTCAGTGACCACTCTACGGTGTCGGGCCTTGAACTACTACCCCCCAGAACATCACCATG AAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCTAAAAGACGTATTG CCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCCCTGGGGAAGAG CAGAGATATACGTNCCAGGTGGAGCACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGG GGTATGTGACTGATGAGAGCCAGGAGCTGAGAAAATCTATTGGGGGGTTGAGAGGAGTGCC TGAGGAGGTAATTATGGCAGTGAGATGAGGATCTGCTCTTTGTTAGGGGGGTGGGCTGAGG GTGGCAATCAAAGGCTTTAACTTGCTTTTTCTGTTTTAGAGCCCTCACCGTCTGGCACCC TAGTACCTCTGCCCCAGGGCACAGTGGGAAGAGGGGCAGAGGGGATCTGGCATCCATGGG TITGCAAGAGCTGTTTAAGGTAGTACAGGGGCTTTGAGGTTGAGAAGTCACTGTGGCTAT TCTCAGAACCCAAATCTGGTAGGGAATGAAATTGATAGCAAGTAAATGTAGTTAAAGAAG ACCCCATGAGGTCCTAAAGCAGGCAGGAAGCAAATGCTTAGGGTGTCAAAGGAAAGAATG TGTTCATAATATTAAGGAAGAGGCAGGGTTCAAGTGAGTAGGAACAAGGGGGAAGTCTCT ATCACATTCAGCTGGGGATCAAGATAGCCTTCTGGATCTTGAAGGAGAAGCTGGATTCCA 5461 5581 5641 5701 5701 5761 5761 5821 5881 5941 1909 6181 6241 6301 6481 5521 5521 5581 5641 5821 5881 5941 6001 6001 6061 6121 6121 6181 6241 6301 6361 6361 6421 6421 6481 6541 QQ Οp qq qq QQ g QQ qq q Q Dp Dp οp Qγ Qγ Ω οy Qγ QΥ οy οy Qγ QΥ δλ Ω q δ Ω δy q Op g οy ò g δ

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	TICACACACGGTGTCCTCCCTAGGCCAGTGCCTCTGGAGTCAGAACTCTGGTGGTATTTC 	CCTCAATGAAGTGGAGTAAGCTCTCTCATTTGAGATGGTATAATGGAAGCCACCAAGTG	GCTTAGAGGATGCCCAGGTCCTTCCATGGAGCCACTGGGGTTCCGGTGCACATTAAAAAA	. AAAATCTAACCAGGACATTCAGGAATTGCTAGATTCTGGGAAATCAGTTCACCATGTTCA 	AAAGAGTCTTTTTTTTTTTTGGGACTCTATTGCCCAGGCTGGAGGTGCAATGGCATGAT 	CTCGGCTCACTGTAACCTCTGCCTCCCAGGTTCAAGCGATTCTCCT	. AGTAGCTGGGATTACAGGCGTGCACCACCATGCCCGGCTAATTTTTGTATTTTTAGTAGA 	. GACAGGGTTTCACCATGTTGGCCAGGCTGGTCTCGAACTCTCCTGACCTCGTGATCGCC	. TGCCTCGGCCTCCCAAAGTGCTGAGATTACAGGTGTGAGCCACCCTGCCCAGCGGTCAAA 	. AGACTCTTAATATATATATCCAGATGGCATGTGTTTACTTTATGTTACTACATGCACTTG 	GCTGCATAAATGTGGTACAAGCATTCTGTCTTGAAGGGCAGGTGCTTCAGGATACCATAT	ACAGCTCAGAAGTITCTTCTTTAGCATTAAATTTTAGCAAGAAGATATCTGATCTCTTCTT 	TTAAACCATTTCTTTTTTGTGGTTAGAAAGTTATGTAGAAAAAGTAATGTGATTT 	ACGCTCATTGTAGAAAAGCTATAAAATGAATACAATTAAAGCTGTTATTAATTA	TGAAAAACTATTAACAACTTGTCTATTACCTGTTAGTATTATTGTTGCTGTTAAAAATGCA 	TATACTITAATAAATGTATATTGTATTGTATACTGCATGATTTTATTGAAGTTCTTGTTCTTTCT	ATCTTGTGTATATATACTTAATCGCTTTGTCATTTTGGAGACATTTATTT	CTTTACATTTTGTCTTACGGAATATTTTCATTCAACTGTGGTAGCCGAATT
8761	8821	8881	8941	9001	9061	9121	9181 9181	9241	9301	9361 9361	9421	9481	9541	9601	9661 9661	9721 9721	9781 9781	9841
, qq	Oy Dp	Qy	Qy Db	Qy Db	Oy Db	Qy	Oy Dp	Oy Dp	Qy Dp	QY Db	Qy Db	Qy Dp	Qy	Qy	Qy	Qy	Qy	οy

10080 10140 10260 10140 10320 10560 10200 CATITIAAATICITATICACCICIGGCAAAACCATICACAAACCAIGGIAGIAAAGAGAA 10380 10500 10500 10560 10620 10680 10740 CTTTACATTTTGTCTTACGGAATATTTTCATTCAACTGTGGTAGCCGAATTAATCGTGTT 9900 TCTTCACTCTAGGGACATTGTCGTCTAAGTTGTAAGACATTGGTTATTTTACCAGCAAAC CATTCTGAAAGCATATGACAAATTATTTCTCTTAATATCTTACTATACTGAAAGCAGA AGGTAAGCATTTGTTTTATATTGGTTTTTATTTCACCTGGGCTGAGATTTCAAGAAACACC CCAGTCTTCACAGTAACACATTTCACTAACACATTTACTAAACATCAGCAACTGTGGCCT GITAATTITITTAATAGAAATTITAAGICCICATTITCCITCGGIGTTTTTTAAGCITAA TTTTTCTGGCTTTATTCATAAATTCTTAAGGTCAACTACATTTGAAAAATCAAAGACCTG GGGTGACACCTGGTGGCCATAGGTAAATGTACCACGGTGGTCCGGTGACCAGAGATGCAG 10561 CTATTTGAATTGCTGGAATCACAGGCCATTGCTGAGCTGCCTGAACTGGGAACACAG AAGGAAAACAAACCACTCTGATAATCATTGAGTCAAGTACAGCAGGTGATTGAGGACTGC 10801 TAAAATCCCCAAATTTTTCATAAAC 10825 10801 TAAAATCCCCAAATTTTTCATAAAC 10825 ь. Sequence 1, Application US/0883
Setent No. 6140305
GENERAL INFORMATION:
APPLICANT: Thomas, Winston US-08-834-497A-1 9961 10381 9901 9901 9961 10321 10621 10021 10081 10141 10141 10201 10201 10261 10321 10501 10501 10021 10081 10261 10381 qq Óγ pp q οy Ω δŽ g δy QΥ Ω q QYQQ οy qq Op Dp ò $Q\underline{y}$ qq QΥ à Db δy g Qγ g δy a δy Db

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LOCATION: 5507...6023
OTHER INFORMATION: /note= "star
OTHER INFORMATION: normal or wi
OTHER INFORMATION: allele (SEQ
FEATURE:
NAME/KEY: allele
LOCATION: replace(3872, "c")
OTHER INFORMATION: /phenotype=
OTHER INFORMATION: (unaffected)
OTHER INFORMATION: /label= 244
FEATURE:
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                             5507..6023
                                                                                                                                                                                                                                                                                                                                                                                      allele
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Matches 10823; Conse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-834-497A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Hereditary Hemochromatosis (HH) gene
allele*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: join(361..436, 3762..4025, 4235..4510, 5606..5881, LOCATION: 6040..6153, 7107..7147)

OTHER INFORMATION: /product- "Hereditary Hemochromatosis OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/ST. - 3891
LOCATION: 3852..3891
OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: normal or wild-type (unaffected) genomic OTHER INFORMATION: sequence surrounding variant for 24d2(C), OTHER INFORMATION: allele (SEQ ID NO:41)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "start and stop positions for normal or wild type (unaffected) allele CDNA (SEQ ID NO:9)"
APPLICANT: Drayna, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Galirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Ruddy, David
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                               ZIP: LUUSO-ZALL
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,497A
FILING DATE: 04-APR-1997
CLASSIFCATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/652,265
FILING DATE: 15-APR-1996
CLASSIFCATION: 514
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION: 514
PRIOR APPLICATION: 514
ATTORNEY AGENT INFORMATION:
NAME: POISSANT, BIAN M.
REGISTRATION NUMBER: 48,907-0056-999
TELECOMMUNICATION INFORMATION:
TELEPAN: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LEMCTH: 10825 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                               3: Pennie & Edmonds LLP
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic) FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: OTHER INFORMATION: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 140..7319
OTHER INFORMATION: ,
OTHER INFORMATION: 1
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                                                                                                                                                                                             STREET: 1155 Aver
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
                                                                                                                                                                                 ADDRESSEE:
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 TCAGGATTTAAAAACCAAGGGGACACTGGATCACCTAGTGTTTCACAAGCAGGTACCTT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTTCCCCGCCCCCAAAAGAAGCGGAGATTTAACGGGGACGTGCGGCCAGAGCTGGGGAA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATGGGCCCGCGAGCCAGGCCGGCGCTTCCCCTGATGCTTTTGCAGACCGCGGTCCTG 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAGGGGCGCCTTGCTGCGTGAGTCCGAGGGCTGCGGGCGAACTAGGGGCGCGCGGGGGTG 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    601 CTACCACTGAACTGCAGATAGGGGTCCCTCGCCCCAGGACCTGCCCCCTCCCCCGGCTGT 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 AATATCTAAAGTTCAGATCAGAACATTGCGAAGCTACTTTCCCCAATCAACAACACCCCT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TCTAAGGTTGAGATAAAATTTTTAAATGATGATGAATTTTGAAAATCATAAAATTTA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TCTAAGGTTGAGATAAAATTTTTAAATGTATGATTGAATTTTGAAAATCATAAATTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 CTGCTGTAGGAGAGAGAACTAAAGTTCTGAAAGACCTGTTGCTTTTCACCAGGAAGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 10825;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
/note= "start and stop positions for
normal or wild-type (unaffected) genomic
sequence surrounding variant for 24d1(G)
allele (SEQ ID NO:20)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                           NAME/KEY: allele
LOCATION: replace(3878, "a")
OTHER INFORMATION: /phenotype= "normal or wild-type
OTHER INFORMATION: (unaffected)"
OTHER INFORMATION: /label= 24d7
                                                                                                                        /phenotype= "normal or wild-type (unaffected)" /label= 24d2
                                                                                                                                                                                                                                                                                                                                                                  LOCATION: replace(5834, "g")
OTHER INFORMATION: 'Thenotype= "normal or wild-type
OTHER INFORMATION: (unaffected)"
OTHER INFORMATION: /label= 2441
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100.0%; Pred. No. 0;
ative 0; Mismatches
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099	720	780	840 840	006	096	1020 1020	1080	1140	1200	1260 1260	1320 1320	1380 1380	1440 1440	1500	1560 1560	1620 1620	1680 1680	1740
	CCCGGCTCTGCGGAGTGACTTTTGGAACCGCCCACTCCCTTCCCCCAACTAGAATGCTTT 	TAAATAAATCTGGTAGTTCCTCACTTGAGCTGAGCTAAGCCTGGGGCTCCTTGAACCTGG	AACTGGGGTTTATTTCCAATGTCAGCTGTGCAGTTTTTTCCCCAGTCATCTCCAAACAGG	AAGTTCTTCCCTGAGTGCTTGCCGAGAAGGCTGAGCAAACCCACAGCAGGATCCGCACGG	GGTTTCCACCTCAGAACGAATGCGTTGGGCGGTGGGGGCGCGAAAGAGTGGCGTTGGGGA 	TCTGAATTCTTCACCATTCCACCACTTTTGGTGAGACCTGGGGTGGAGGTCTCTAGGGT 	GGGAGGCTCCTGAGAGAGGCCTACCTCGGGCCTTTCCCCACTCTTGGCAATTGTTCTTTT	GCCTGGAAAATTAAGTATATGTTAGTTTTGAACGTTTGAACTGAACAATTCTCTTTTCG 	CTAGGCTFTATTGATTTGCAATGTGCTGTGTAATTAAGAGGCCTCTCTACAAAGTACTGA 	TAATGAACATGTAAGCAATGCACTCCAACTTCTAAGTTACATTCATATCTGATCTTATTTGA 	TITICACIAGGCATAGGGAGGTAGGAGCTAATAATACGTTTATITTACTAGAAGTTAACT 	GGAATTCAGATTATATAACTCTTTTCAGGTTACAAAGAACATAAATAA	ATGTTATTTCAAGTACTACAGCTGCTTCTAATCTTAGTTGACAGTGATTTTGCCCTGTAG	TGTAGCACAGTGTTCTGTGGGTCACGCCGGCCTCAGCAGCAGCACTTTGGTATTTGGTA	CTACGTGTATCCACATTTTACACATGACAAGAATGAGGCATGGCACGGCCTCCTTCCT	CAAATTTATTCAATGGTACACTGGGCTTTGGTGGCAGAGCTCATGTCTCCACTTCATAGC	TATGATTCTTAAACATCACACTGCATTAGAGGTTGAATAATAAATTTCATGTTGAGCAGIIIIIIIIII	AAATATTCATTGTTTACAAGTGTAAATGAGTCCCAGCCATGTGTTGCACTGTTCAAGCCC
601	661	721	781	841	901	961	1021	1081	1141	1201	1261	1321	1381	1441	1501	1561	1621	1681
, q	QY	Oy Dp	Qy Db	Qy Dp	Oy Db	Qy Dp	QY Dp	Qy Db	Qy Db	Qy Db	Qy	QY	Qy Dp	Qy Dp	QY DP	Qy Dp	Qy Db	δλ

qq	1681	AAATATTCATTGTTTACAAGTGTAAATGAGTCCCAGCCATGTGTTGCACTGTTCAAGCCC 1740
ογ	1741	3GGAGAGAGCAGGGAAACAAGTCTTTACCCTTTGATATTTTGCATTCTAGTGGGAGA 1
qq	1741	AAGGGAGAGGAGGAAACAAGTCTTTACCCTTTGATTTTTGCATTCTAGTGGGAGA 1
Qy	1801	ATGACAATAAGCAAATGAGCAGAAAGATATACAACATCAGGAAATCATGGGTGTTGTGA 186
QΩ	1801	SACAATAAGCAAATGAGCAGAAAGATATACAACATCAGGAAATCATGGGTGTTGTGA 1
δy	1861	GAAGCAGAGAAGTCAGGGCAAGTCACTCTGGGGCTGACACTTGAGCAGAACATGAAGGA 1920
qq	1861	Sagagaagtcagggcaagtcactctggggctgacacttgaggcagaagaa 192
δλ	1921	98
qa	1921	AAGAATGATATTGACTGGGAGCAGTATTTCCCAGGCAAACTGAGTGGGCCTGGCAAG 198
Qy	1981	04
qq	1981	TGGATTAAAAAGCGGGTTTTCTCAGCACTACTCATGTGTGTG
Qy	2041	10
qa	2041	seceredededededededededededededededededed
QY	0	9
QQ	2101	CTCCCTACTCACTAGGTGCTAGGAGCACTCCCCCAGTCTTGACAACCAAAAAATGTCTCT
Qy Ph	2161	AAACTTTGCCACATGTCACCTAGTAGACAAACTCCTGGTTAAGAAGCTCGGGTTGAAAA 2220
3 3	9 6	OCC
QV	7 7	######################################
œ C	77	GIGCTGGGGGGTAGAGGCCAAGAAGTAGGTAATGGGGCTCAGAAGAGGG ZZB
Qy		GCCACAAACAAGGTTGTGCAGGCGCTGTAGGCTGTGGTGTGAATTCTAGCCAAGGAGTA 2340
Q Q	o V	ACAAACAAGGIIGIGCAGGCCIGIAGGCIGIGGAAIICIAGCCAAGGAGIA 234
yo da	2341	ACAGTGATCTGTCACAGGCTTTTAAAAGATTGCTCTGGCTGCTATGTGGAAAGCAAAG 2400
3 8	, (246
ξ q	40	ANGOSACCAACAGTAAAAACAACAGGGGAGCCCAGCCAGGGAAGGTACAACAGTACAACAAACA
QY	2461	3TAGTGGAGTGGGCTGGGTGGGAACAGAAAAAGGGAGTGACAAACCATTGTCTCT
QO	2461	
Qy	2521	ATATTCTGAAGGAAGTTGCTGAAGGATTCTATGTTGTGTGAGGAGAAAGAGAAATTGG 258
qq	2521	TCTGAAGGAAGTTGCTGAAGGATTCTATGTTGTGTGAGAAAGAA
Qy	2581	CTGGGTGTAGTAGCTCATGCCAAGGAGGCCAAGGAGAGCAGATTCCTGAGCTCAGGA 2640
qq	2581	IGGGTGTAGTAGCTCATGCCAAGGAGGAGGCCAAGGAGCAGAGTTCCTGAGCTCAGGA 26
οy	2641	GITCAAGACCAGCCTGGGCAACACAGCAAAACCCCTTCTCTACAAAAAATAA 2700
qa	2641	TTCAAGACCAGCCTGGGCAACACCAGCAAAACCCCTTCTCTACAAAAATACAAAAATT
QY	2701	GCTGGGTGGTGGAGCACCTGTGATCCTAGCTACTCGGAGGCTGAGGTGGAGGTTA 2760
qq	2701	CTGGGTGTGGCATGCACCTGTGATCCTAGCTACTCGGGAGGCTGAGGTGGAGGGT
δy	2761	TTGCTTCAGCCCAGGAAGTTGAGGCTGCAGTGAGCCATGACTGTGCCACTGTACTTCAGC 2820
qu	2761	TGCTTGAGCCCAGGAAGTTGAGGCTGCAGTGAGCCATGACTGTGCCACTGTACTT

SGTGACAGAGCAAGACCCTGTCTCCCCTGACCCCTGAAAAAGAGAAGAGTTAAAGT 2880 	STITGITCITIAITITAAITITAATGGCCTGAGCAGGGGGGAATTGGCAATGCCAT 2940 	ICAGATGGTGAAGGCAGAGAAAGAGCAGTTTGGGGTAAATCAAGGATCTGCATTTG 3000 	CATGITAAGITIGAGATICCAGICAGGCITCCAAGIGGIGAGGCCACAIAGGCAGI 3060 	IGTAAGAATTCAGGACCAAGGCTGGGCACGGTGGCTCACTTCTGTAATCCCAGCACT 3120 	TGGCTGAGGCAGGTAGATCATTTGAGGTCAGGAGTTTGAGACAAGCTTGGCCAACA 318 	TGAAACCCCATGTCTACTAAAAATACAAAAATTAGCCTGGTGTGGTGGGGGGCACGCCT 3240 	GTCCCAGGTTTTCAGGAGGCTTAGGTAGGAGAATCCCTTGAACCCAGGAGGTGCAGG 3300 	CAGTGAGCTGAGATTGTGCCACTGCACTCCAGCCTGGTGATAGAGTGAGT	aaaaaaaaaaaaaaaaaaaaaaaaactgaaggaattattcctcaggatttggg 3420 	AATTIGCCCTGAGCACCAACTCCTGAGTTCAACTACCATGGCTAGACACACTTAAC 3480 	TTCTAGAATCC TTCTAGAATCC	GGGGCAGTGAGGGGTGGCAGCCACGTGTGGCAGAAAAGCACACAGAGAAAGAA	CAGGACTGTCATATGGAAGAAAGACAGGACTGCAACTCACCTTCACAAAATGAGGA 3660 	GACACAGCTGATGGTATGAGTTGATGCAGGTGTGTGGAGCCTCAACATCCTGCTCCC 3720 	CCTACTACACATGGTTAAGGCCTGTTGCTCTCCAGGTTCACACTCTCTGCACTA 3780 	CCTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCTTGTTTGAAGCTTTGGGCTA 3840 	Ŭ − (
CTAGGTG CTAGGTG	₽-₽	<-<	Ē-Ē		5 – 5	« — «	υ-υ	(2) — (2)	CTCAAA CTCAAA	TCTAAT: TCTAAT:	5 - 5	999	8=8	AGAC - - AGAC	⊢ − ⊢	달드달	CGTGGA
2821 C	2881	2941	3001 (3061 (3121	3181	3241	3301	3361	3421	3481	3541	3601	3661	3721	3781	3841
Oy Op	Oy Db	Oy Db	Qy Dp	oy Dp	Qy Db	Qy Dp	Oy Dp	oy op	Qy Dp	Qy	Qy	67 67	Qy Dp	Oy Db	Oy Dp	Oy Dp	ઠે તે

4680 4740 4800 5040 4620 4680 4740 4800 4860 4860 4920 4920 4980 4980 4200 4440 4440 4560 4560 4620 4260 4320 4320 4380 4380 4500 4500 4080 4140 4200 GCTAATTGGAAGGCTGAGGCAGGAGCATCGCTTGAACCTGGGAAGCGGAAGTTGCACTGA AAATICAGAAATGTCAAGGCCGGGCACGGTGGCTCACCCCTGTAATCCCAGCACTTTGGG AAATTCAGAAATGTCAAGGCCGGGCACGGTGGCTCACCCCTGTAATCCCAGCACTTTGGG ACCCGTCTCTAAAAAATACAAAATTAGCTGGTCACAGTCATGCGCACCTGTAGTCCCA AGGCCGAGGCGGGTGGTCACAAGGTCAGGAGTTTGAGACCAGCCTGACCAACATGGTGAA CAGGACCACCTTGAATTCTGCCCTGACACACTGGATTGGAGGAGCAGCAGAACCCAGGGCC TGGCCCACCAAGCTGGAGAAAGGCACAAAGATTCGGGCCAGGCAGAACAGGGCCTAC AGGTTGCAGGGCACGGAATCCCTGGTTGGAGTTTCAGAGGTGGCTGAGGCTGTGTGCCTC ATGCATCTTGAAGGAAACAGCTGGAAGTCTGAGGTCTTGTGGGAGCAGGAAAGAGGGAAG GAATTTGCTTCCTGAGATCATTTGGTCCTTGGGGATGGTGGAAATAGGGACCTATTCCTT GGCTGTGAAAATGCAAGAAGACAACAGTACCGAGGGCTACTGGAAGTACGGGTATGATGGG 4801 4861 4621 4681 4681 4741 4741 4801 4921 4981 4441 4561 4621 4861 4921 4261 4321 4381 4441 4081 4141 4201 4201 4261 4321 4021 4081 4141 3901 3901 3961 3961 4021 g QQ pp δ ò QY Db q Óλ qq οy Qγ Q g QΥ 엄 δy g Qγ QQ g Q δλ QQ Qγ Ob QΥ g δy g Qγ qq Óγ δŽ ò Ω

GCCAAGATCGAAGCCAGGAAGCATCGCTTGAACCTGGGAAGCGGAAGCTGGAAGTGGAAGTCGCAAGATCGAAGTCGCAAGATCAGGAATCAGAAAAAAAA	CCAAGAGGCAGGGGGGGGGGGGGGGGGGGGGGGGGGGG		GTGAGACTCCATCTTAAAAA 510 	TCATATGAATACCAGGACAAA 5160 	TAGGTTAAAAGTTTCTTTCAT 5220 	CGCTTCTTATAACAATGC 528 	CATTTTCAATGCACATAA 534 	4847476747477476476 5400 	GTGTTAGAGTCCAATCTTAGG 5460 	GAAAAGGGTATTTCCTTCCC 5520 	CCAGGGTAAACAGATCCCCTCTC 5580 	4 4	PACCCCCAGAACATCACCATG 5700	TCGAACCTAAAGACGTATTG 5760 	GCTGTACCCCCTGGGGAAGAG 5820 	CAGCCCTCATTGTGATCTGG 5880 	3C 594	TGTTAGGGGTGGGCTGAGG 6000 	**************************************
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đ	6061	TAGTCATTGGAGTCATCAGTGGAATTGCTGTTTTTGTCGTCATCTTGTTCATTGGAATTT	6120
QY	6121	TGTTCATAATATTAAAGGAAGGCAGGCTTCAAGTGAGTAGGAACAAGGGGGAAGTCTC	
qq	6121		6180
Qy	6181	TAGTACCTCTGCCCCAGGGCACAGTGGGAAGAGGGGCCAGAGGGGGATCTGGCATCCATGG	6240
QQ	6181	TAGTACCTCTGCCCCAGGGCACAGTGGGAAGAGGGGCAGAGGGGATCTGGCATCGG	6240
QY	24	AAGCATTTTCTCATTTATATTCTTGGGGACACCAGCAGCTCCCTGGGAGACAGAAAAT	Ō
q Q	24	AAGCATTTTTCTCATTTATATTCTTTGGGGACACCCAGCAGCTCCCTGGGAGAGAAAT	6300
Qy Db	6301	AATGGTTCTCCCCAGAATGAAGTCTCTAATTCAACAACATCTTCAGAGCACCTACTAT 	36
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d _U	36.	TTTGCAAGACTGTTTAAGGTAGTACAGGGCTTTGAGGTTGAGAAGTCACTGTGGCTAT TTTGCAAGAGCTGTTTAAGGTAGTACAGGGCTTTTGAGGTTGAGAAGTCACTGTGGCTAT	6420
Qy	6421	CTCAGAACCCAAATCTGGTAGGGAATGAAATTGATAGCAAGTAAATGTAGTTAAAGAAG	6480
Dβ	6421		æ
Qy	6481	GTCCTAAAAGCAGGAAGCAAATGCTTAGGGTGTCAAAGGAAAGAATG	6540
QQ	6481	CCCATGAGGTCCTAAAGCAGGCAGGAAGCAAATGCTTAGGGTGTCAAAGGAAAGAATG	6540
QY	54	ATCACATTCAGCTGGGGATCAGATAGCCTTCTGGATCTTGAAGGAGAAAGCTGGATTCCA (9
an an	U.	JACATTCAGCTGGGGATCAAGATAGCCTTCTGGATCTTGAAGGAGAGCTGGATTCCA (0099
ογ	09	TTAGGTGAGGTTGAAGATGATGGAGGTCTACACACAGACGGAGCAACCATGCCAAGTAGA (0999
qq	6601	FTCAGGTTGAAGATGATGGGAGGTCTACACAGACGGAGCAACCATGCCAAGTAGGA	99
Qy	6661	GAGTATAAGGCATACTGGGAGATTAGAAATAATTACTGTACCTTAACCCTGAGTTTGCGT	6720
QQ	6661	NTAAGGCATACTGGGAGATTAGAAATAATTACTGTACCTTAACCCTGAGTTTGCGT	~
QY	6721		
QQ	6721	GCTATCACTCACCAATTATGCATTTCTACCCCCTGAACATCTGTGGTGTAGGGAAAAAAA	6780
ΟŊ	6781	TTGGGATATTGGGTTATGA	6840
qq	6781	AATCAGAAAGAAGCCAGCTCATACAGAGTCCAAGGGTCTTTTGGGATATTGGGTTATGA	4
Qy	6841	SAAAGGAGGACCACGATCTCCCTTATATGGTG	0069
qq	6841	CACTGGGGTGTCTTGAAGGATCCTAAGAAAGGAGGACCACGATCTCCCTTATATGGTG	0
Qy	6901	SAAAGCCAATAAGCAT	0969
qa	6901	STGTTGTTAAGAAGGTAGATGAGGTGAGGAGACCAGGTAGAAAGCCAATAAGCAT	9
Οy	6961	CCAGATGAGAGATAATGGTTCTTGAAATCCAATAGTGCCCAGGTCTAAATTGAGATGG	7020
q 0	1969	TCCAGATGAGAGATAATGGTTCTTGAAATCCAATAGTGCCCAGGTCTAAATTGAGATGG	7020
Qy	7021	SAGAGAAGAGGCAAGATGGTGCCTAGGTTTGTGATGCCT	7080
qq	7021	3AATGAGGAAAATAAGGAAGAGAGAGAGGCAAGATGGTGCCTAGGTTTGTGATGCCT	08
Qy	7081	CACAGGAGGAGCCATGGGGCACTACGTCTTAGCTGAACG	7140
qq	7081	TCCTGGGTCTCTTGTCTCCACAGGAGCACCATGGGGCACTACGTCTTAGCTGAACG	7140
Οy	14	TGAGTGACACGCAGCCTGCAGACTCACTGTGGGAAGGAGACAAAACTAGAGACTCAAAGA 7	7200
qq	7141	GAGTGACACGCAGCCTGCAGACTCACTGTGGGAAGGAGAAAAAAAA	7200

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7201	7261	7321	7381	7441	7501	7561	7621 7621	7681 7681	7741	7801	7861	7921	7981	8041	8101	8161 8161	8221
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qq	281 ACGCC	GTAGTCCCAGCTACTCGGAAGGCTGAGGCAGGAGATGGCATGAACCCAGGAGG 8
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QY	61 TAGAG	ATCTCATAGITIGICAGICAIAGAAACAGGITTCAAACTCAGICAATCIGACG 8
QQ	— ř	AAACAGGTTTCAAACTCAGTCAATCTGACCG 8
δλ	521 TTTGA	AGTAGTTTAGATGCCTAGAATAAATAGAGAA 8
qq	TTGA	racatctcagacaccactacattcagtagtttagatgcctagaataaata
δỳ	GGAAG	3AGATGGCTCTTCTCTTGTCTCATTGTGTTCTTCTGAGTGAG
Dβ	SAAG	BAGATGGCTCTTCTCTTGTCTCATTGTGTTTCTTCTGAGTGAG
Οy	41 GAAGG	GAACAGCAGAAAACAACCAACTGATCCTCAGCTGTCATGTTTCCTTTAAAAGTC #
q	41 GAA	GAACAGCAGAAAAAAACCAACTGATCCTCAGCTGTCATGTTTGCTTTAAAAGTC B
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οp	:E	SGAAGGTCCTGGAATGTGACTCCCTTGCTCCTCTGTTGCTCTTTTGGCATTCA E
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qq	- ⊟	TTGGACCCTACGCAAGGACTGTAATTGGTGGGGACAGCTAGTGGCCCTGCTGGGC
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QQ	- 5	Acedigicoreceradeceagreereregagreagacereregererarite 888
Qγ	8881 CCTCA	GAGTEGAGTAACCTCTCTCATTTGAGATGGTATAATGGAAGCCACCAAGTG 894
qq	CTC	SAAGTGGAGTAAGCTCTCTCATTTTGAGATGGTATAATGGAAGCCACCAAGTG 894
QY	941 GCTT	36atgcccaggrcctrccargagcccactggggtrccgcrccactaaaaa 9
Q	CIL	GGATGCCCAGGTCCTTCCATGGAGCCACTGGGGTTCCGGTGCACATTAAAAAA 900
δλ	<i>a</i> –	Jaaccaggacattcaggaattgctagattctgggaaatcagttcaccatgttca 906
QC	9001 AAAAT	STAACCAGGACATTCAGGAATTGCTAGATTCTGGGAAATCAGTTCACCATGTTCA 90
QY	9061 AAAGA	STCTTTTTTTTTTTGAGACTCTATTGCCCAGGCTGGAGTGCAATGCCATGAT 4
QQ	- 17	STCTTTTTTTTTTTTGAGACTCTATTGCCCAGGCTGGAGTGCAATGGCATGAT 91
Οy	9121 CTCGG	CTCACTGTAACCTCTGCGTCCCAGGTTCAAGCGATTCTCCTGTCTCAGCCTCCCA 91
qq	- Ö	crearigraaccierecereceagricaagearierecigrereageereea 91
ΟŸ	9181 AGTAG	CIGGGATTACAGGCGTGCACCACCATGCCCGGCTAATTTTTGTATTTTTAGTAGA 924
QQ	81 AGT	CIGGGATTACAGGCGTGCACCACCATGCCCGGCTAATTTTTGTATTTTTAGTAGA 924
QY	9241 GACAG	GGTTTCACCATGTTGGCCAGGCTGGTCTCGAACTCTCCTGACCTCGTGATCCGCC 930
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οy	9301 TGCCT	CGGCCTCCCAAAGTGCTGAGATTACAGGTGTGAGCCACCCTGCCCAGCCGTCAAA 936
QQ	01 TGCC	CGGCCTCCCAAAGTGCTGAGATTACAGGTGTGAGCCACCCTGCCCAGCCGTCAAA 936
Qy	9361 AGAGT	CTTAATATATATATCCAGATGGCATGTGTTTACTTTATGTTACTACATGCACTTG 9420

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	948	ATCTCTTCTT 9540 ATCTCTTCTT 9540	AATGTGATTT 9600 AATGTGATTT 9600	AATTAGCCAG 9660 AATTAGCCAG 9660		31TCTTGTTC 9780 3TTCTTGTTC 9780	CTTCTAATTT 9840 		ACCAGCAAAC 9960 CCAGCAAAC 9960		TAATTTATT 10080 TAATTTATT 10080	AAGAAACACC 10140 AGAAACACC 10140	CTGTGGCCT 10200 CTGTGGCCT 10200	10260 	AAAGACCTG 10320 AAAGACCTG 10320	TAAAGAGAA 10380 TAAAGAGAA 10380	GAGATGCAG 10440 GAGATGCAG 10440	GCACTGGAA 10500
	GCTGCATAAATGTGGTACAAGCATTCTGTCTGAAGGGCAGGTGCTTCAGGATACCATAT 	ACAGCTCAGAAGTTTCTTTTAGGCATTAAATTTTAGCAAAGATATCTCATCTCTTCTT 	TTAAACCATTTTCTTTTTTGTGGTTAGAAAAGTTATGTAGAAAAAGTAAATGTGATTT 	acgctcattgtagaaaagctataaaatgaatacaattaaaagctgttatttaattagccag 	TGAAAAACTATTAACAACTTGTCTATTACCTGTTAGTATTATTGTTGCATTAAAAATGCA 	TATACTTTAATAAATGTATATTGTATTGTATACTGCATGATTTTATTGAAGTTCTTGTTC 	apcitgegralatacitaatcgcittgicattitggagacatttattiggegcitciaatti 	CTTPACATTTGCTTACGGAATATTTCATTCAACTGTGGTAGCGGAATTAATCGTGT 	TCTTCACTCTAGGGACATTGTCGTCTAAGTTGTAAGACATTGGTTATTTTACCAGCAAC 	CATTCTGAAAGCATATGACAAATTATTCTCTCTTAATATCTTACTACTATACTGAAAGCAGA 	CTGCTATAAGGCTTCACTTACTCTTCTACCTCATAAGGAATATGTTACAATTAATT	AGGTAAGCATTTGTTTTATATTGGTTTTATTTCACCTGGGCTGAGATTTCAAGAACACC 	CCAGTCTTCACAGTAACACATTTCACTAACACATTTACTAAAACATCAGCAACTGTGGCCT 	GTTAATTTTTTAATAGAAATTTTAAGTCCTCATTTTCTTTGGGGGTTTTTTAAGCTTAA 	TTTTTCTGGCTTTATTCABAAATTCTTAAGGTCAACTACATTTGAAAAATCAAGACCTG 	CATTTTAAATTCTTATTCACCTCTGGCAAAACCATTCACAAACCATGGTAGTAAAGAGAA 	GGGTGACACCTGGTGGCCATAGGTAAATGTACCACGGTGGTCCGGTGACCAGAGATGCAG 	CGCTGAGGGTTTCCTGAAGGTAAAGGAATAAAGAATGGGTGGAGGGGCGTGCACTGGAA
					-			CTTTACATTTTGTCTTACGG	TCTTCACTCTAGGGACATTG:	CATTCTGAAAGCATATGACAI 	CTGCTATAAGGCTTCACTTAC	AGGTAAGCATTTGTTTTATATATATATATATATATATATA	CCAGTCTTCACAGTAACACAT	GTTAATTTTTTAATAGAAAT 	TTTTCTGGCTTTATTCATAP 	CATTTTAAATTCTTATTCACC	GGGTGACACCTGGTGGCCATA 	CGCTGAGGGTTTTCCTGAAGG
9361	9421	9481	9541	9601	9661	9721	9781 9781	9841	9901	9961	10021	10081	10141	10201	10261	10321	10381 10381	10441
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10441 CGCTGAGGGTTTTCCTGAAGGTAAAGGAATAAAGAATGGGTGGAGGGGCGTGCACTGGAA 10500
                                         TGAGAGGTACAGGCCAAAATTCTTATGTTGTATTATAATAATGTCATCTTATAATACTGT 10740
                                                                                                                                                                                                                                                                                                        10741 CAGTATTTTATAAAACATTCTTCACAAACTCACACATTTAAAAACAAAACACTGTCTC 10800
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Patent No. 6140305

GENERAL INFORMATION

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APPLICANT: Ruddy, David

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APPLICANT: Tsuchhashi, Zenta

APPLICANT: Wolff, Roger K.

TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS

NUMBER OF SEQUENCES: 76

CORRESPONDENCES: Pennie & Edmonds LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONFESTIONERS E Educates LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STREET: New York
STATE: New York
COUNTRY: USA
2 LP: 10036-2811
COMPUTER: NEW BORK
COMPUTER: READABLE FORM:
MEDIUM TYPE: FloPPY disk
COMPUTER: READABLE FORM:
MEDIUM TYPE: FloPPY disk
COMPUTER: READABLE FORM:
MEDIUM TYPE: OMPORER: NEW OF WINDOWS 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,497A
FILING DATE: 04-APR-1997
CLASSIFICATION ST4
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/652,265
CLASSIFICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
CLASSIFICATION ST4
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
CLASSIFICATION: 514
APPLICATION NUMBER: US 08/630,912
FILING DATE: 104-APR-1996
CLASSIFICATION: ST4
APPLICATION NUMBER: US 08/630,912
FILING DATE: 104-APR-1996
CLASSIFICATION: ST4
ATTORNEY/AGENT INFORMATION:
NAME: POISSAIL, BRIAM M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 28,907-0056-999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 10825;
                                                                                                                                                LOCATION: join(361..436, 3762..4025, 4235..4510, 5606..5881, LOCATION: 6040..6153, 7107..7147)

COTHER INFORMATION: /product= "Hereditary Hemochromatosis OTHER INFORMATION: muttation"

OTHER INFORMATION: /nuttation"

OTHER INFORMATION: /note= "Hereditary Hemochromatosis (HH)

OTHER INFORMATION: /note= "Hereditary Hemochromatosis (HH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /phenotype= "Hereditary Hemochromatosis
                                                                                                                                                                                                                                                                                                NAMENTER: -
LOCATION: 3852..3891

LOCATION: 7 Anote= "start and stop positions for OTHER INFORMATION: 4 genomic sequence surrounding variant OTHER INFORMATION: for 24d2(C) allele (SEQ ID NO:41)"
                                                                                                                                                                                                                                                                                                                                                                                            /note= "start and stop positions for genomic sequence surrounding variant for 24d1(A) allele (SEQ ID NO:21)"
                                                                                                                                                                                                                                                                 for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
                                                                                                                                                                                                                                                     LOCATION: 140..7319
OTHER INFORMATION: /note- "start and stop positions
OTHER INFORMATION: 24d1 allele cDNA (SEQ ID NO:10)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 10823; Ded. No. 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label- 24d1
                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
LOCATION: 5507..6023
COTHER INFORMATION: /note="star
OTHER INFORMATION: genomic sequ
OTHER INFORMATION: for 24d1(A)
FEATURE:
NAME/KEY: allele
LOCATION: replace(5834, "a")
OTHER INFORMATION: /phenotype=
OTHER INFORMATION: /label= 24d1
ILLEPHONE: 650-493-4935
TELERAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 10825 base pairs
TYPE: nucleic acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 10823; Conservative
                                                                                                                MOLECULE TYPE: DNA (genomic) FEATURE:
                                                                                                       linear
                                                                                                                                       NAME/KEY: CDS
                                                                                                                                                                                                                                           NAME/KEY:
                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-834-497A-3
                                                                                                                                                                                                                                 EATURE:
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TTTTCACTAGGCATAGGGAGGTAGGAGCTAATAATACGTTTATTTTACTAGAAGTTAACT 1320
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                                                                                                                                                                                                                                                                                 780
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                                                                                                                                                                                                                               TAAATAAATCTCGTAGTTCCTCACTTGAGCTGAGCTAAAGCCTGGGGCTCCTTGAACCTGG
                                                                                                                                                                                                                                                                                                AAGTICITCCCTGAGTGCTTGCCGAGAAGGCTGAGCAAACCCACAGGAGGATCCGCACGG
                                                                                                                                                                                                                                                                                                                                                                                                   TCTGAATTCTTCACCCATTCCACCTTTTGGTGAGACCTGGGGTGGAGGTCTTAGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGGAGGCTCCTGAGAGAGGCCTACCTCGGCCTTTCCCCACTCTTGGCAATTGTTCTTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TAATGAACATGTAAGCAATGCACTCACTTCTAAGTTACATTCATATCTGATCTTATTTGA
                                                                                                                                                                                                                                                                                                                                     AACTCGGGTTTATTTCCAATGTCAGCTGTGCAGTTTTTTCCCCAGTCATCTCCAAACAGG
                                       361 ATGGGCCCGCGAGCCAGGCCGGCGTTCTCCTCCTGATGCTTTTGCAGACCGCGGTCCTG
                                                                           GAAAAATCGAAACTAGCTTTTCTTTGCGCTTGGGAGTTTGCTAACTTTGGAGGACCTGC
                                                                                         TCAACCCTATCCGCAAGCCCCTCTCCCTACTTTCTGCGTCCAGACCCCGTGAGGGAGTGC
                        CAGGGGCGCTTGCTGCGTGAGTCCGAGGGCTGCGGGGGGACTAGGGGCGCGCGGGGGTG
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g 2	4	STANDARD STA	
Qy Dp	1501	CTACGTGTATCCACATTTTACACATGACAAGAATGAGGCATGGCACGCCTGCTTCCTGG 1560 	
Qy Dp	1561 1561	CAAAITIATICAAIGGIACACIGGGCITIGGIGGCAGAGCICAIGITCICCACITCAIAGC 1620 	
Qy Dp	1621 1621	TATGATICTTAAACATCACACTGCATTAGAGGTTGAATAATAAATTTCATGTTGAGCAG 1680 	
Qy Db	1681	CACTGTTCAAGCCC 1	
QY	1741	CAAGGGAGAGAGGGAAACAAGTCTTTACCCTTTGATATTTTGCATTCTAGTGGGAGA 1800 	
oy O	1801	GATGACAATAAGCAAATGAGCAGAAAGATATACAACATCAGGAAATCATGGGTGTTGTGA 1860 	
OY Db	1861	GAAGCAGAGAAGTCAGGGCAAGTCACTCTGGGGCTGACACTTGAGCAGAGACATGAAGGA 1920 	
Qy Db	1921 1921	AATAAGAATGATATTGACTGGGAGCAGTATTTCCCCAGGCAAACTGAGTGGGCCTGGCAAG 1980 	
Qy Db	1981 1981	TTGGATTAAAAAGGGGGTTTTCTCAGCACTACTCATGTGTGTG	
QY Db	2041	CGGCGTGGGGGTGGGAAGGGGACTACCATCTGCATGTAGGATGTCTAGCAGTATCCTGT 2100	
Oy Dp	2101	2 2	
Oy Db	2161	AAACTITGCCACAIGTCACCIAGIAGACAAACTCCTGGTIAAGAAGCTCGGGTTGAAAAA 2220 	
Qy Dp	2221	AATAAACAAGTAGTGCTGGGGAGTAGAGGCCAAGAAGTAGGTAATGGGCTCAGAAGAGGA 2280 	
Qy Db	2281	GCCACAAACAAGGTTGTGCAGGCGCTGTAGGCTGTGGTGTGAATTCTAGCCAAGGAGTA 2340 	
Qy Db	2341	ACAGTGATCTGTCACAGGCTTTTAAAAGATTGCTCTGGCTGCTATGTGGAAAGCAGAATG 2400	
Qy Db	2401	AAGGGAGCAACAGTAAAAGCAGGGAGCCCAGCCAGGAAGCTGTTACACAGTCCAGGCAAG 2460 	
Qy	2461	AGGTAGTGGAGTGGGTGGGAACAGAAAGGGAGTGACAAACCATTGTCTCCTGAA 2520 	
Οy	52	ATATTCTGAAGGAAGTTGCTGAAGGATTCTATGTTGTGTGAGAGAAAAAAAA	

2700 2760 2700 2760 2820 2820 2880 2940 3000 3120 3120 3180 3180 3240 3240 3300 3420 3420 3480 3660 GCTGGGTGTGGCATGCACCTGTGATCCTAGCTACTCGGGAGGCTGAGGTGGAGGGTA GTTCAAGACCAGCCTGGGCAACACACAAAACCCCTTCTCTACAAAAATACAAAATTA ACCCAGGACTGTCATATGGAAGAAGACAGGACTGCAACTCACCCTTCACAAAATGAGGA CTGGGTGTAGTAGCTCATGCCAAGGAGGAGGCCAAGGAGAGAGCAGATTCCTGAGCA CTAGGTGACAGAGCAAGACCCTGTCTCCCCTGACCCCCTGAAAAAGAGAAGAGTTAAAGT TGACTITGITCITITATITITAATITITATIGGCCTGAGCGAGTGGGGTAATITGGCAATGCCAT TTCTGAGATGGTGAAGGCAGAAAGAGCAGTTTGGGGTAAATCAAGGATCTGCATTTG GGACATGTTAAGTTTGAGATTCCAGTCAGGCTTCCAAGTGGTGAGGCCACATAGGCAGTT CAGTGTAAGAATTCAGGACCAAGGCTGGCACGGTGGCTCACTTCTGTAATCCCAGCACT TTGGTGGCTGAGGCAGGTAGATCATTTGAGGTCAGGAGTTTGAGACAAGCTTGGCCAACA TCTAATTTGCCCTGAGCACCAACTCCTGAGTTCAACTACCATGGCTAGACACACCTTAAC TGGTGAAACCCCCATGTCTACTAAAAATACAAAATTAGCCTGGTGTGTGGCGCCCCCT ATAGTCCCAGGTTTTCAGGAGGCTTAGGTAGGAGAATCCCTTGAACCCAGGAGGTGCAGG ATTTTCTAGAATCCACCAGCTTTAGTGGAGTCTGTCTAATCATGAGTATTGGAATAGGAT 2581 2641 2701 2761 2821 2881 3001 3061 3181 3181 3241 3361 3421 2521 2581 2641 2701 2761 2821 2881 2941 2941 3001 3061 3121 3121 3241 3301 3301 3361 3421 3481 3481 3541 3541 3601 qq Dρ QY qq QΥ δy Q g Dp q οy QΥ οy δ g QY QQ δý Qγ Db QQ g QY qq q qq Qγ δŽ δ Qγ ŏ qq Qγ g δ

3660 3720 3720 3780 3780 3840 3840	96 96 02 02 0	4080 4080 4140 4140 4200	4260 4260 4320 4320 4380	4440 4440 4500 4500 4560	4620 4620 4680 4680 4740
ACCCAGGACTGTCATATGGAAGAAGACAGGACTGCAACTCACCCTTCACAAAATGAGGA CCAGACACAGGTGATGGTATGATTGATGCAGGTGTGGAGGCTCCACCTTCACAAAATGAGGA [111111111111111111111111111111111		CAAGGGTATGGGGGGGCCTCACCTCGGGGTTGTCGGGAGTTTTTCACTTTTCACTTTTCACTTTTCACTTTTCACTTTTTT	### TOTTGCAGTTAACAAGGCTGGGGATTTTTCCAGAGTCCCACACCCTGCAGGTCATCTG	TGGCCCACCAAGCTGGAGTGGGAAAGGCACAAGATTCGGGCCAGGCAGAACAGGGCCTAC	TTGCAGGCACGGAATCCCTGGTTGGAGTTTCAC
3601 3661 3721 3721 3781 3781	96	4021 4021 4081 4081 4141	4201 4201 4261 4321 4321	4381 4381 4441 4501 4501	4561 4561 4621 4621 4681
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5520 5640 5400 5460 5460 5520 5580 5580 5760 5760 5340 5700 5700 5040 5100 5100 5340 5400 GCCAAGATCGCGCCACTGCACTCCAGCCTAGGCAGAGAGTGAACTCCATTAAAAAA AGAACATAGCAATAATCACTGAAGCTACCTATCATACAAGTCGGCTTCTTATAACAATGC TCTTCAGTGACCACTCTACGGTGTCGGCCCTTGAACTACTCCCCCAGAACATCACCATG CCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCCCCGGGGAAGAG CCCAATGGGGATGGGACCTACCAGGGTGGATAACCTTGGCTGTACCCCCTGGGGAAGAG GCCAAGATCGCGCCACTGCACTCCAGCCTAGGCAGAGTGAGACTCCATCTTAAAAAA **AAAAAAAAAAAAAAAAAAGAGAATTCAGAGATCTCAGCTATCATATGAATACCAGGACAAA** AGGGCAATTTTATCTATCAGAACAAGAACATGGGTAACAGATATGTATTTACATGTG AGGAGAACAAGCTGATCTGACTGCTCTCCAAGTGACACTGTGTTAGAGTCCAATCTTAGG CICAICCIICCITICCIGICAAGIGCCICCIIIIGGIGAAGGIGACACAICAIGIGACC AAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCTAAAAGACGTATTG AAATTCAGAAATGTCAAGGCCGGGCACGGTGGCTCACCCCTGTAATCCCAGCACTTTGGG AGGCCGAGGCGGGTCACAAGGTCAGGAGTTTGAGACCAGCCTGACCAACATGGTGAA 5641 5641 5761 4981 5041 5101 5161 5161 5221 5221 5281 5281 5341 5341 5401 5461 5461 5521 5521 5581 5581 5701 5701 5761 4741 4801 4801 4861 4861 4921 4921 4981 5041 5101 5401 4741 g Dp g qq Qγ g δŽ QQ òγ Ω Qγ g ŏ g δy g QΥ Db οy qq QΥ q Ω Ob Qγ Db qq g οy Q QΥ δy Qγ ΟŽ ò δ

5880	94	000	090	120 120	യ യ	240 240	300	360	420 420	480 480	540 540	900	560	720	780	840 840	006	ت د
1 CAGAGATATACGTNCCAGGTGGAGCACCCAGGCCTGGATCAGCCCTCATTGTGATCTGG	1. GGTATGTGACTGAGAGAGCAGGAGCTGAGAAATCTATTGGGGGTTGAGAGGAGTGC 5	1 TGAGGAGGTAATTATGGCAGTGAGATGAGGATCTGCTCTTTGTTAGGGGGTGGGCTGAGG 6	1. GTGGCAATCAAAGGCTTTAACTTGCTTTTTTGTGTTTTAGAGCCCTCACCGTCTGGCACCC 6	1 TAGTCATTGGAGTCATCAGTGGAATTGCTGTTTTTTGTCGTCATCTGTTCP	1 IGTTCATAATATTAAGGAAGAGGCAGGGTTCAAGTGAGTAGGAACAAGGGGGAAGTCTCT 	1 TAGTACCTCTGCCCCAGGGCACAGTGGGAAGGGGGCAGAGGGGATCTGGCATCCATGGG 6	1 AAGCATTTTTCTCATTTATATTCTTTGGGGACACCAGCAGCTCCTGGGAGACAGAAAT 6	1 AATGGTTCTCCCCGGAATGAAAGTCTCTAATTCAACAAACA	1 TITGCAAGAGCTGTTTAAGGTAGTACAGGGGCTTTGAGGTTGAGAAGTCACTGTGGCTAT 6	1 TCTCAGAACCCAAATCTGGTAGGGAATGAAATTGATAGCAAGTAAATGTAGTTAAAGAAG 6	1 ACCCCATGAGGTCCTAAAGCAGGCAGGAAGCAAATGCTTAGGGTGTCAAAGGAAAGAATG 6	1 ATCACATTCAGCTGGGGATCAAGATAGCCTTCTGGATCTTGAAGGAGAAGCTGGATTCCA 6	1 TTAGGTGAGGTTGAAGATGAGGGGGGGGGTCTACACAGACGAGCAAGCCATGCCAAGTAGGA 6	GAGTATAAGGCATACTGGGAGATTAGAAATAATTACTGTACCTTAACCCTGAGTTTGGGT 6	AGCTATCACTCACCAATTATGCATTTCTACCCCTGAACATCTGTGGTGTAGGGAAAAGA 6	GAATCAGAAAGAAGCCAGCTCATACAGAGTCCAAGGGTCTTTTGGGATATTGGGTTATGA 6	TCACTGGGGTGTCATTGAAGGATCCTAAGAAAGGAGGACCACGATCTCCCTTATATGGTG 6	AAIGIGITGITAAGAAGITAGAIGAGAGGIGAGGAGACCAGITAGAAAGCCAAIAAGCA 6
582	588	594	600	6062	6121	6181	6241	6301	6361	6421	6481	6541 6541	6601	6661	6721 6721	6781 6781	6841 6841	6901
Òy Db	Qy	QY Db	Qy	Qy Db	Oy Db	Qy	Qy	Qy	Q _Y	Qy Db	Qy	Qy Db	Qy Dp	Oy Dp	Oy Db	Qy Db	Qy Dp	Qγ

0969 7020 7080 7140 7140 7200 7200 7260 7260 7320 7320 7440 7440 7380 7380 7500 7500 7560 7560 7620 7620 7680 7680 7740 7740 7800 7800 7860 7920 7920 8040 CTTTCCTGGGTCTCTTGTCTCCACAGGAGGAGCCATGGGGGCACTACGTCTTAGCTGAACG TGAGTGACACGCAGCCTGCAGACTCACTGTGGGAAGGAGACAAAACTAGAGACTCAAAGA GGGAGTGCATTTATGAGCTCTTCATGTTTCAGGAGAGAGTTGAACCTAAACATA GTGAATGAGGAAAATAAGGAAGAGAAGAGGCAAGATGGTGCCTAGGTTTGTGATGCCT GCCTGACGAACTCCTTGATTTTAGCCTTCTCTGTTCATTTCCTCAAAAAATTTCCCCAT TTAGGTTTCTGAGTTCCTGCATGCCGGTGATCCCTAGCTGTGACCTCTCCCCTGGAACTG CTTACATGATTCATTTTAACATCTGAGAAAAGCTTTGAACCCTGGGACGTGGCTAGTCAT CATCTGATTGTGATGTGAGTTGCACAGCTATGAAGGCTGTACACTGCACGAATGGAAGAG ATTATGATAAGGATGATAAAAGCACTTACTTCGTGTCCGACTCTTCTGAGCACCTACTAA **ACATACACCTATGTCATTTCCTATTTTTGGAAGAGGACTCCTTAAATTTGGGGGA** TTGAATCCTCTCTCTGTGTTACCCAGTAACTCATCTGTCACCAAGCCTTGGGGATTCTTC GCACCTGTCCCAGAAAAAGCATCATGGCTATCTGTGGGTAGTATGATGGGTGTTTTTAGC AGGTGTCATACAGATTTGCAAAGTTTAATGGTGCCTTCATTTGGGATGCTACTCAAGTAT TCCAGACCTGAAGAATCACAATAATTTTCTACCTGGTCTCTCCTTGTTCTGATAATGAAA **AACCITACCAGATTTTTACACATGTATCTATGCATTTTTCTGGACCCGTTCAACTTTTCCT** 6961 1969 7021 7741 (6901 7021 7081 7081 7141 7201 7201 7261 7261 7321 7321 7381 7381 7441 7441 7501 7501 7561 7561 7621 7681 7621 7741 7801 7861 7681 7801 7861 7921 7921 7981 Qγ q Qγ g ΩY q òγ g Óλ qq g qq g qq ŏ Qγ Óλ Ω δ qq Óγ g δ g δy d δ q δ pp g Ω ò δ ŏ

8040	8100 8100	8160 8160	8220 8220	8280	8340	8400	8460 8460	8520 8520	8580 8580	8640 8640	8700 8700	8760 8760	8820 8820	8880	8940	0006	0906	9120 9120
ATTATGATAAGGATGATAAAAGCACTTACTTCGTGTCCGACTCTTCTGAGCACCTACTTA	CATGCATTACTGCATGCACTTCTTACAATAATTCTATGAGATAGGTACTATTATCCCCAT	TTCTTTTTAAATGAAGAAAGTGAAGTAGGCCGGGCACGGTGGCTCACGCCTGTAATCCC	AGCACITIGGGAGGCCAAAGCGGGTGGATCACGAGGTCAGGAGATCGAGACCATCCTGGC	TAACATGGTGAAACCCCATCTCTAATAAAAATACAAAAAATTAGCTGGGCGTGGTGGGCGT 	CGCCTGTAGTCCCAGCTACTCGGAAGGCTGAGGCAGGAGAATGGCATGAACCCAGGA 	AACCTTGCAGTGAGCCGAGTTTGCGCCACTGCACTCCAGCCTAGGT 	CTCCATCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	TAGAGTATCTCATAGTTTGTCAGTGATAGAAACAGGTTTCAAACTCAGTCAATCTGACCG 	TTGATACATCTCAGACACCACTACATTCAGTAGTTTAK 	GGAAGGAGATGGCTCTTCTTGTCTCATTGTGTTTCTTCTGAGTGAG	GAACAG GGAACAG	CCTGAAGGAAGGTCCTGGAATGTGACTCCCTTGCTCCTCTTTGCTCTCTTTGGCATTCA	TTTCTTTGGACCCTACGCAAGGACTGTAATTGGTGGGGACAGCTAGTGGCCCTGCTGGC 	TCACACA TCACACA	5=5		AAAATCTAACCA 	AAAGAGTCTTTTTTTTTT
7981	8041	8101	8161 8161	8221	2 28	34	8401	8461	in in	8581 8581	8641	8701	8761 8761	8821	8881	8941	9001	9061
qq	oy Db	Oy Dp	Oy Db	. yo	δ Q	oy Dp	oy op	Qy	Oy Dp	oy Ob	Oy Dp	Oy Dp	Qy	Oy Dp	Qy Dp	Qy Db	Qy Dp	. 상 면

10020 10140 10200 10080 9840 9840 0066 0066 0966 9780 9600 0996 0996 9720 9720 9780 9180 9240 9300 9360 9420 9420 9480 9480 9540 AGGTAAGCATTTGTTTTATATTTGGTTTTTATTTCACCTGGGCTGAGATTTCAAGAAACACC CCAGTCTTCACAGTAACACATTTCACTAACACTTTACTAAACATCAGCAACTGTGGCCCT TATACTTTAATAAATGTATATTGTATTGTATACTGCATGATTTTATTGAAGTTCTTGTTC CTTTACATTTTGTCTTACGGAATATTTTCATTCAACTGTGGTAGCCGAATTAATCGTGTT GCTGCATAAATGTGGTACAAGCATTCTGTCTTGAAGGGCAGGTGCTTCAGGATACCATAT AGAGTCTTAATATATATCCAGATGGCATGTGTTTACTTTATGTTACTACATGCACTTG TGCCTCGGCCTCCCAAAGTGCTGAGATTACAGGTGTGAGCCACCCTGCCCAGCCGTCAAA 9841 9841 9901 9961 10021 10021 10081 9781 9961 10141 9601 9661 1996 9721 9721 9781 10081 10141 9241 9361 9361 9421 9481 9481 9541 9541 9601 9901 9121 9181 9181 9241 9301 9301 9421 9121 g 셤 9 Qγ δy g qq q QΥ qq Q δ qq οy QQ ΟY Q Ω Ω Óγ g Qγ οqα Q qq δ Qγ ò Q qq ò Op δy Ω ò

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61 AATATCTAAAGTTCAGATCAGAACATTGCGAAGCTACTTTCCCCAATCAACAACACCCCT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TCTAAGGTTGAGATAAAATTTTTAAATGTATGATTGAATTTTGAAAATCATAAATTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: join(361..436, 3762..4025, 4235..4510, 5606..5881, LOCATION: join(361..436, 3762..4025, 4235..4510, 5606..5881, LOCATION: 6040..6153, 7107..7147)

OTHER INFORMATION: /Product= "Hereditary Hemochromatosis OTHER INFORMATION: mutation: autation: oTHER INFORMATION: // note= "Hereditary Hemochromatosis (HH) OTHER INFORMATION: gene 24d2 allele"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 3; Length 10825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: replace(3872, "g")
COTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis OTHER INFORMATION:
OTHER INFORMATION: /label= 24d2
US-08-834-497A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: - COMPATION: 3852..3891
OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: genomic sequence surrounding variant OTHER INFORMATION: for 24d2(G) allele (SEQ ID NO:42)" FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "start and stop positions for
genomic sequence surrounding variant
for 24d1(G) allele (SEQ ID NO:20)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: /note= "start and stop positions OTHER INFORMATION: 24d2 allele cDNA (SEQ ID NO:11)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 10823; 100.0%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                 8907-0056-999
                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
CLASSIFICATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
CLASSIFICATION: 514
         FILING DATE: 04-APR-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-WAY-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic) FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 10825 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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Matches 10823; Conservative
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OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: FRATURE:
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                     GGGTGACACCTGGTGGCCATAGGTAAATGTACCACGGTGGTCCGGTGACCAGACATGCAG 10440
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MEDUUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
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STREET: 1155 Avenue of the Americas
CIIY: New York
STATE: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
APPLICANT: Thomas, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K
TITLE OF INVENTION: HEREDITARY H
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
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1980 1980 2040 2040 2100 2100 2160 AACAAGTAGTGCTGGGGAGTAGAGGCCAAGAAGTAGGTAATGGGCTCAGAAGAGGA 2280 1740 1800 1800 1860 1920 1680 CAGAGAAGTCAGGGCAAGTCACTCTGGGGCTGACACTTGAGCAGAGACATGAAGGA 1920 TTTGCCACATGTCACCTAGTAGACAAACTCCTGGTTAAGAAGCTCGGGTTGAAAAA 2220 1380 1380 1440 1500 1560 1620 1620 1680 ACAATAAGCAAATGAGCAGAAAGATATACAACATCAGGAAATCATGGGTGTTGTGA 1860 CITTATIGATITGCAAIGIGCIGIGIAATIAAGAGGCCICICIACAAAGIACTGA 1200 TTTATTCAATGGTACACTGGGCTTTTGGTGGCAGAGCTCATGTCTCCACTTCATAGC AGAATGATATTGACTGGGAGCAGTATTTCCCAGGCAAACTGAGTGGGCCTGGCAAG CCTACTCACTAGGTGCTAGGAGCACTCCCCCAGTCTTGACAACCAAAAATGTCTCT ACTAGGCATAGGGAGGTAGGAGCTAATAATACGTTTATTTTACTAGAAGTTAACT SCACAGTGTTCTGTGGGTCACACGCCGGCCTCAGCACAGCACTTTGAGTTTTGGTA STGTATCCACATTTTACACATGACAAGAATGAGGCATGGCACGGCCTGCTTCCTGG ATTCTTAAACATCACACTGCATTAGAGGTTGAATAAAAATTTCATGTTGAGCAG

2340	2400	2460	2520	2580	2640 2640	2700	2760 2760	2820 2820	2880	2940	3000	3060	3120	3180	3240 3240	3300	3360
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2281	2341	2401	2461	2521 2521	2581 2581	2641	2701	2761 2761	2821 2821	2881	2941	3001	3061	3121	3181	3241	3301
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qq	Oy Db	Qy	Oy Db	Oy Dp	Qy Db	Qy Dp	Q D	Oy Dp	Oy Dp	Oy Db	Qy Db	Oy Db	Qy Db	Qy Db	Oy Db	Qy Db	Oy Db	Oy

5580 5700 5700 5760 5760 5820 5880 5880 5940 0009 6000 0909 0909 6120 6120 6180 6180 6240 6240 6300 6300 6360 6360 6420 6420 6480 6480 6540 6540 9600 0099 0999 **ACCCCATGAGGTCCTAAAGCAGGCAGGAAGCAAATGCTTAGGGTGTCAAAGGAAAGAATG** ATCACATTCAGCTGGGGATCAAGATAGCCTTCTGGATCTTGAAGGAGAAGCTGGATTCCA TAGTACCTCTGCCCCAGGGCACAGTGGGAAGAGGGGGCAGAGGGGGATCTGGCATCCATGGG TITICCAAGAGCTGTTTAAGGTAGTACAGGGGCTTTGAGGTTGAGAAGTCACTGTGGCTAT TCTCAGAACCCAAATCTGGTAGGGAATGAAATTGATAGCAAGTAAATGTAAAGAAG TCTTCAGTGACCACTCTACGGTGTCGGGCCTTGAACTACTACCCCCCAGAACATCACCATG AAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCTAAAGACGTATTG GTGGCAATCAAAGGCTTTAACTTGCTTTTTTCTGTTTTAGAGCCCTCACCGTCTGGCACCC AACCTATAGAAGGAAGTGAAAGTTCCAGTCTTCCTGGCAAGGGTAAACAGATCCCCTCTC CAGAGATATACGTNCCAGGTGGAGCACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGG TGAGGAGGTAATTATGGCAGTGAGATGAGGATCTGCTCTTTGTTAGGGGGTGGGCTGAGG GIGGCAATCAAAGGCTTTAACTTGCTTTTTTTTTTAGAGCCCTCACCGTCTGGCACCC 5641 5821 5881 5941 6001 6061 6061 6121 6121 6181 6181 6241 6301 6361 6481 6541 6541 6601 6601 5521 5581 5581 5641 5701 5701 5761 5761 5821 5881 5941 6001 6241 6301 6361 6421 6421 6481 QQ Db qq q g q QQ δy qq g δy Db οy Db g Dp QQ g Dp οy δ δy οy Qγ δ 임 Qγ g ÓΥ Dp οy δ ōλ δy οy ο̈́λ οy

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	11 GCACCTGTCCCAGAAAAGCATCATGGCTATCTGTGGGTAGTATGATGGTGTTTTTAGC 78
78(01 aggtaggaggcaatatcttgaaaggggttgtgaagaggtgttttttctaattggcatga 78
78.	61 AGGTGTCATACAGATTTGCAAAGTTTAATGGTGCCTTCATTTGGGATGCTACTCTAGTAT 79
.97 YC	21 TCCAGACCTGAAGAATCACAATAATTTTCTACCTGGTCTCTCCTTGTTCTGATAATGAAA 79 11
2y 79	81 ATTATGATAAGGATGATAAAAGCACTTACTTCGTGTCCGACTCTTCTGAGCACCTACTTA 80
QY 80. Db 80.	41 CATGCATTACTGCATGCACTTCTTACAATAATTCTATGAGATAGGTACTATTATCCCCAT 81
Qy 81. Db 81	01 TTCTTTTTAAATGAAGAAAGTGAAGTAGGCCGGGCACGGTGGCTCACGCCTGTAATCCC 81
Qy 81 Db 81	61 AGCACITIGGGAGGCCAAAGCGGGTGGATCACGAGGTCAGGAGATCGAGACCATCCTGGC 82
2y 82 Db 82	21 TAACATGGTGAAACCCCATCTCTAATAAA
2y 82 Db 82	ACGCCTGTAGTCCCAGCTACTCGGAAGGCTGAGGCAGGAGAAATGGCATGAACCCAGGAGG 8:
2y 83 Db 83	1 CAGAGCTIGCAGTGAGCCGAGTTIGCGCCACTGCACCTAGCCGAGGTGAGA 84
2y 84 Db 84	01 CTCCATCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
Oy 84 Db 84	61 TAGAGTATCTCATAGTTTGTCAGTGATAGAACAGGTTTCAAACTCAGTCAATCTGACCG
Qy 85 Db 85	21 TITGATACATCTCAGACACCACTACATTCAGTAGTTTAGATGCCTAGAATAAATA
Qy 85 Db 85	81 GGAAGGAGATGGCTCTTCTCTTGTCTCATTGTGTTTCTTCTGAGTGAG
Qy 86 Db 86	3GAACAGCAGAAAACAACTGATCCTCAGCTGTCATGTTTCCTTTAAAAGTC 8701
78 YC	01 CCTGAAGGAAGGTCCTGGAATGTGACTCCCTTGTTGTTGTTGTTTTTTGGCATTCA 876
Oy 87	61 TTTCTTTGGACCCTACGCAAGGACTGTAATTGGTGGGGACAGCTAGTGGCCCTGCTGGGG 8
- σ	21 TICACACACGGTGTCCTCCCTAGGCCAGTGCCTCTGGAGTCAGAACTCTGGTGGTATTTC 88

8880 8940 8940 9000 9060	9120 9120 9180 9180 9240 9300	3 3 6 4 4 2 3 6 4 4 2 5 4 1 5	9600 9600 9660 9720 9720 9780	9840 9840 9900 9900
	AAAGAGTCTTTTTTTTTTTTTGAGACTCTATTGCCCAGGCTGGAGTGCAATGGCATGAT	TCGGCCTCCCAAAGTGCTGAGATTACAGGTGTGAGCCACCCTGCCAGCCGTCAA	TTAAACCATTTCTTTTTTGGGTTAGAAAGTTATGTAGAAAAAGTAAATGTGATTT	ATCTTGTGTATATACTTAATCGCTTTGTCATTTTGGAGACATTTATTT
8821 8881 8841 8941 8941 9001	9061 9061 9121 9121 9181 9241	9301 9301 9361 9421 9421 9481	9541 9541 9601 9661 9661 9721	9781 9781 9841 9841
00 OX	6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	6	60 60 60 60 60 60 60 60 60 60 60 60 60 6	oy oy oy.

10080 10200 10140 10200 10020 10080 10140 10260 10320 CATITITAAATICTITATICACCICIGGCAAAACCATICACAAACCATGGTAAAAGAGAA 10380 10440 10620 10800 10440 10500 10560 CTATITIGAATIGCIGGAATCACAGGCCATIGCIGAGCIGCCIGAACIGGGAACACAACAG 10620 10680 10680 10740 9901 TCTTCACTCTAGGGACATTGTCGTCTAAGTTGTAAGACATTGGTTATTTTACCAGGAAAC 9960 CATTCTGAAAGCATATGACAAATTATTTCTCTTTAATATCTTACTATACTGAAAGCAGA 9961 CATTCTGAAAGCATATGACAAAATTATTTCTCTTAATATCTTACTATACTGAAAGCAGA CCAGTCTTCACAGTAACACATTTCACTAACACTTTACTAAACATCAGCAACTGTGGCCT GITAATTITITAATAGAAATTITAAGTCCTCATTITCTTTCGGTGTTTTTAAGCTTAA TITITICTGGCTTTATTCATAAATTCTTAAGGTCAACTACATTTGAAAAATCAAAGACCTG CGCTGAGGGTTTTCCTGAAGGTAAAGGAATAAAGAATGGGTGGAGGGGCGTGCACTGGAA AAGGAAAACAAACCACTCTGATAATCATTGAGTCAAGTACAGCAGGTGATTGAGGACTGC 10741 CAGTATTTTATAAAACATTCTTCACAAACTCACACACATTTAAAAACAAAACACTGTCTC 10801 TAAAATCCCCAAATTTTTCATAAAC 10825 10021 1966 10381 10441 10141 10141 10201 10201 10261 10321 10321 10381 10441 10501 10501 10561 10561 10621 10621 10801 δ g ò q Qγ g δy Db Dp δy g q Ω QΫ́ ò οy Db δy g qq qq q οy Qγ ò òγ qq ò g ò

RESULT 8
US-08-834-97A-7
Sequence 7, Application US/08834497A
Patent No. 6140305
GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
APPLICANT: Drayna, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Ruddy, Andreas
APPLICANT: Ruddy, David

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Db
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LOCATION: join(361..436, 3762..4025, 4235..4510, 5606..5881,
LOCATION: 6040..6153, 7107..7147)
COTHER INFORMATION: /Product= "Hereditary Hemochromatosis
OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: GRecontaining a combination of both OTHER INFORMATION: gene containing a combination of both OTHER INFORMATION: 24d1 and 24d2 alleless"
                         NUMBER OF INVENTION: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Hereditary Hemochromatosis (HH)
gene containing a combination of both
24d1 and 24d2 alleles"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "start and stop positions for CDNA containing a combination of both 24d1 and 24d2 alleles (SEQ ID No:12)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: genomic sequence surrounding variant OTHER INFORMATION: for 24d2(G) allele (SEQ ID NO:42)"
                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPATING SYSTEM: Windows 95
SOFTWARE: Fast-SEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8907-0056-999
                                                                                            E: Pennie & Edmonds LLP
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/834,497A FILING DATE: 04-APR-1997 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-PR-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INPORMATION:
NAME: POISSANT, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-
TELECOMMUNICATION INFORMATION:
TELEFAM: 650-493-4935
TELEFAM: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 7:
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: HEREDITARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 10825 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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NAME/KEY:
LOCATION: 140..7319

OTHER INFORMATION: CD
                                                                      CORRESPONDENCE ADDRESS:
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LOCATION: 3852..3891
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OTHER INFORMATION:
                                                                                                          STREET: 1155 Aver
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2811
                                                                                                                                                                                                                                                                                                                                       FILING DATE: 04
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LOCATION:
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 AATATCTAAAGTTCAGATCAGAACATTGCGAAGCTACTTTCCCCAAATCAACAACACCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 TCAGGATTTAAAAACCAAGGGGACACTGGATCACCTAGTGTTTCACAAGCAGGTACCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 TTTCCCCGCCCCCCAAAAGAAGGGGAGATTTAACGGGGGACGTGCGGCCAGAGCTGGGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      361 ATGGCCCCGCGAGCCAGGCCGGCGCTTCTCCTCTGATGCTTTTGCAGACCGCGGTCCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAAAAATCGAAACTAGCTTTTTCTTTGCGCTTGGGAGTTTGCTAACTTTGGAGGACCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            601 CTACCACTGAACTGCAGATAGGGGTCCCTCGCCCCAGGACCTGCCCCCTCCCCCGGCTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   541 TCAACCCTATCCGCAAGCCCCTCTCCCTACTTTCTGCGTCCAGACCCCGTGAGGGAGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 10825;
                                                                                                                                                                                                                                                                            3872, "g")
/Phenotype= "Hereditary Hemochromatosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /phenotype= "Hereditary Hemochromatosis
/note= "start and stop positions for genomic sequence surrounding variant for 24dl(A) allele (SEQ ID NO:21)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 10823;
Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= 24d2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= 24d1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARLON: replace(5834, "a")

COTHER INFORMATION:

CO
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100.0%;
                                                                                               OTHER INFORMATION: for 24th of the control of the c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0
Matches 10823; Conservative
                                                           INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181
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AACTCGGGTTTATTCCAATGTCAGCTGTGCAGTTTTTTCCCCAGTCATCTCCAAACAGG [CCTGGAAATTAAGTATATGTTAGTTTTGA 	AATGAACATGTAACCAATGCACTCACTTCT AATGAACATGTAAGCAATGCACTCACTTCT TTCACTAGGCATAGGAGTAGGAGTAGGAGTAGGATAGGA	TTCAGATTATARA 		CAAATTTATTCAATGGTACACTGGGCTTTGGTGGCAGAGCTCATGTCTCCACTTCATAGC [PATTCATTGTTTACAAGTGTAAATGAGTCCCAGCCATGTGTTGCACTGTTCAAGCC 	CAAGGAGAGAGAGAAACAAGTCTTTACCCTTTGATTTTGCATTCTAGTGGGAGAGAGA
781 781 841 841 901	961 961 1021 1021	1081 1081 1141	0 0 9	1321 1321 1381 1381	1441 1441 1501 1501	1561 1561 1621 1621	1681	74 74 80 80
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Qy	1861	GAAGCAGAGAAGTCAGGGCAAGTCACTCTGGGGCTGACACTTGAGCAGAGACATGAAGGA 1 	1920
Qy	1921	AATAAGAATGATATTGACTGGGAGCAGTATTTCCCAGGCAAACTGAGTGGGCCTGGCAAG 	1980
Qy	1981	TTGGATTAAAAAGCGGGTTTTCTCAGCACTACTCATGTGTGTG	2040
Qy		CGGCGTGGGGGTGGGAACTACCATCTGCATGTAGGATGTCTAGCAGATACCTGT :	2100
Qy Dp	2101	CCTCCCTACTCACTCAGGGGCACTCCCCCAGTCTTGACAACCAAAAATGTCTCT :	2160
QY Db	2161	AAACTTTGCCACATGTCACCTAGTAGACAAACTCCTGGTTAAGAAGCTCGGGTTGAAAA :	2220
Qy Dp	2221	AATAAACAAGTAGTGCTGGGGAGTAGAGGCCAAGAAGTAGGTAATGGGCTCAGAAGAGG :	80 80
Qy	2281	GCCACAAACAAGGTTGTGCAGGCGCTGTAGGCTGTGGTGTAATTCTAGCCAAGGAGTA :	2340
Qy Dp	2341	ACAGTGATCTGTCACAGGCTTTTAAAAGATTGCTCTGGCTGCTATGTGGAAAGCAGAATG	2400
Qy Db	2401	AAGGGAGCAACAGTAAAAGCAGGGAGCCCAGCCAGGAAGCTGTTACACAGTCCAGGCAAG	2460
Qy	2461	AGGTAGTGGAGTGGGCTGGGTAACAGAAAGGGAGTGACAAACCATTGTCTCCTGAA 	2520 2520
Qy	2521	TATATTCTGAAGGAAGTTGCTGAAGGATTCTATGTTGTGTGAGAGAAGAAGAAGAATTGG 	œ œ
QY	2581	CTGGGTGTAGTAGCTCATGCCAAGGAGGAGCCAAGGAGAGCAGATTCCTGAGCTCAGGA	64 64
QY Db	2641	GITCAAGACCAGCCTGGGCAACACAGCAAAAACCCCTTCTCTACAAAAAATTACAAAAATTA 	
QY	2701	GCTGGGTGTGGTGGCATGCACCTGTGATCCTAGCTACTCGGGAGGCTGAGGTGGAGGGTA	2760 2760
Qy	2761 2761	TTGCTTGAGCCCAGGAAGTTGAGCTGCAGTGAGCCATGACTGTGCCACTGTACTTCAGC	2820
Qy	2821	CTAGGTGACAGAGCAAGACCTGTCTCCCCTGACCCCTGAAAAAGAGAAGAAGTTAAAGT	2880
Qy	2881	TGACTTTGTTCTTTATTTTAATTTTATTGCCTGAGCAGTGGGGTAATTGGCCATGCCATGCCATGCCATGCCATGCCATGCCATGCCATGCCATGCCTTGTTGTTTTAATTGCCCTGAGCAGTGGGGGTAATTGGCCATGCCATGGCCATGGCATGCATG	2940
Qy	2941	. TTCTGAGATGGTGAAGGCAGAGGAAAGAGCAGTTTGGGGTAAATCAAGGATCTGCATTTG	3000

	GGCCACATAGGCAGTT 3060 	CTGTAATCCCAGCACT 3120 		31GGTGGCGCACGCCT 3240	(7 (7	RAGAGTGAGACTCTGT 3360 	TTCCTCAGGATTTGG 3420 	CTAGACACCTTAAC 3480 	AGTATTGGAATAGGAT 3540 	ZACACAAGGAAAGAGC 3600 	TTTCACAAAATGAGGA 3660 	COACATCTGCTCCC 3720	JACACTCTGCACTA 3780 	TGAAGCTTTGGGCTA 3840 	91GTGGAGCCCCGAAC 3900 	GAGTCAGAGTCTGAA 3960 	NAAATCACAACCACAG 4020 	AGCTTTTCATCTTTC 4080
	GGACATGTTAAGTTTGAGATTCCAGTCAGGCTTCCAAGTGGTGAG 	CAGTGTAAGAATTCAGGACCAAGGCTGGGCACGGTGGCTCACTTGT	TTGGTGGCTGAGGCAGGTAGATCATTTGAGGTCAGGAGTTTGAGACAAGCTT 	TGGTGAAACCCCATGTCTACTAAAAATACAAAAATTAGCCTGGTGTGGTGGCGTGGTGGTGTGGTGGCTGGTGGGGGG	ATAGTCCCAGGTTTTCAGGAGGCTTAGGTAGGAGAATCCCTTGAACCCAGGAGGT 	TIGCAGIGAGCIGAGAIIGIGCCACIGCACICCAGCCIGGGIGAIAGAGIGAG. 	CTCAAAAAAAAAAAAAAAAAAAAAAAAAAAACTGAAGGAATTATTCCTCA 	TCTAATTTGCCCTGAGCACCAACTCCTGAGTTCAACTACCATGGCTAGACACACCT"	ATTTCTAGAATCCACCAGCTTTAGTGGAGTCTGTCTAATCATGAGTATTGGAATAG	CTGGGGGCAGTGAGGGGGTGGCAGCCACGTGTGGCAGAGAAAAGCACACAAGAAAAGC 	ACCCAGGACTGTCATATGGAAGAAGACAGGACTGCAACTCACCCTTCACAAAATGAGGA 	CCAGACACAGCTGATGGTATGAGTTGATGCAGGTGTGTGGAGCCTCAACAT	CTCCTACTACACATGGTTAAGGCCTGTTGCTCTGTCTCCAGGTTCACACTCT	CCTCTICATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCTTGTTTGAAGCTTTGGC 	CGTGGATGACCAGCTGTTCGTGTTCTATGATNATGAGAGTCGCCGTGTGTGAGCCC 	TCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGCAGCTGAGTCAGAGT 	AGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTATGGAAAATCACACACA	CAAGGGTATGTGGAGAGGGGCCTCACCTTCCTGAGGTTGTCAGAGCTTTTCATCTTTTC
2941	3001	3061	3121	3181	3241	3301	3361	3421	3481	3541	3601 3601	3661 3661	3721 3721	3781 3781	3841	3901 3901	3961 3961	4021
, QQ	Qy	Qy	QY Db	Qy Db	Qy	Oy Dp	Qy Db	Oy Db	Qy	QY Db	Qy Db	QY	oy Db	Qy Db	oy Ob	oy Db	Qy Db	QY

4320 4320 4380 4500 4560 4560 4620 4680 4740 4740 4800 4800 4860 4860 5040 5100 5160 CAAGGGTATGTGGAGAGGGGCCTCACCTTCCTGAGGTTGTCAGAGCTTTTCATCTTTTC 4080 5160 AGGCCGAGGCGGGTGGTCACAAGGTCAGGAGTTTGAGACCAGCCTGACCAACATGGTGAA GCCAAGATCGCGCCACTGCACTCCAGCCTAGGCAGCAGAGTGAGACTCCATTAAAAA ATGCATCTTGAAGGAAACAGCTGGAAGTCTGAGGTCTTGTGGGGAGCAGGGAAGAAG GAATTTGCTTCCTGAGATCATTTGGTCCTTGGGGGATGGTGGAAATAGGGACCTATTCCTT CTGGAGAGGGACTGCCCTGCACAGCTGCAGCTGCTGGAGCTGGGGGAGAGGTGTTTTG GACCAACAAGGTATGGTGGAAACACATTCTGCCCCTATACTCTAGTGGCAGAGTGGAGG AGGTTGCAGGGCACGGAATCCCTGGTTGGAGTTTCAGAGGTGGCTGAGGCTGTGTGCCTC TGAGACAGCCACAAGTCATGGGTTTAATTTCTTTTCTCCATGCATATGGCTCAAAGGGAA GTGTCTATGCCCTTGCTTTTATTTAACCAATAATCTTTTGTATATTATACCTGTTAA AAATTCAGAAATGTCAAGGCCGGGCACGGTGGCTCACCCCTGTAATCCCCAGCACTTTGGG ACCCGTCTCTAAAAAAAAAAATTAGCTGGTCACAGTCATGCGCACCTGTAGTCCCA TGGTTGCAGTTAACAAGGCTGGGGATTTTTCCAGAGTCCCACACCCTGCAGGTCATCCTG GGCTGTGAAATGCAAGAAGACAGTACCGAGGGCTACTGGAAGTACGGGTATGATGGG TGGCCCACCAAGCTGGAGTGGGAAAGGCACAAGATTCGGGCCAGGCAGAACAGGGCCTAC GCTAATTGGAAGGCTGAGGCAGGAGCATCGCTTGAACCTGGGAAGCGGAAGTTGCACTGA GCCAAGATCGCGCCACTGCACTCCAGCCTAGGCAGCAGAGTGAGACTCCATCTTAAAAAA 4381 4681 4801 4021 4081 4081 4141 4141 4201 4201 4261 4321 4321 4381 4441 4501 4501 4561 4621 4681 4741 4741 4801 4861 4921 4261 4441 4561 4621 4861 4921 5041 4981 4981 5041 Ω g δy g QY Dp Qγ q δy g δŽ g Qγ qq οy q δ g δ Ω δy qq QΣ Db δý g δ qq QΥ d ŏ QQ δ g ò q

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ATATCAAGTGAGGCCACTTATCAGAGTAGAAGATCCTTTAGGTTAAAAGTTTCTTTC	GGGCAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	AACCTATAGAAGGAAGTGAAAGTTCCAGTCTTCCTGGCAAGGGTAAACAGATCCCCTCTC	TCTTCAGTGACCACTCTACGGTGTCGGGCCTTGAACTACCCCCAGAACATCACCATG	CCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCCCTGGGGAAGAG [GTGGCAATCAAAGGCTTTAACTTGCTTTTTCTGTTTTAGAGCCCTCACCGTCTGGCACCC [TGTTCATAATATTAAGGAAGGCAGGGTTCAAGTGAGTAGGAACAAGGGGGAAGTCTCT
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OY 10621 AAGGAAACAAACCACTCTGATAATCATTGAGTCAAGTACAGCAGTGATTGAGGACTGC 10680		MUMBER OF SEQUENCES: 44 CORRESPONDENCE ADDRESS: ADDRESSEE: Pennie & Edmonds LLP STREET: 1155 Avenue of the Americas CITY: New York STATE: New York COUNTRY: USA IP: 10036 COMPUTER READABLE FORM: MEDIUM TYPE: Ploppy disk COMPUTER READABLE FORM: MEDIUM TYPE: Ploppy disk COMPUTER: 18M PC Compatible OPERATING SYSTEM: Windows 95 SOFTWARE: Worderfect Version 8 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/503,444A STILING DATE: 14 FEb-200 CLASSIFICATION: PROPERTION: PRIOR APPLICATION UMBER: 08/652,265 FILING DATE: 23-May-1996 SPIOR APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: 08/632,673 FILING DATE: 13-May-1996 SPIOR APPLICATION DATA: APPLIC	FILIN DATE: 10.74PI 1990 PRIOR APPLICATION DARE: 08/630,912 APPLICATION NUMBER: 08/630,912 FILING DATE: 04.4pI-1996 ATTORNEY/AGENT INPORMATION: NAME: POISSANT, Brian M. REGISTRATION NUMBER: 28,462 REGISTRATION NUMBER: 28,462 RELECHONE: 212-790-999 TELEPHONE: 212-790 TELEPHONE:
9541 TTAAACCATTTTCTTTTTTTGGGTTAGAAAGTTATGTAGAAAAAAGGTAATGTGATTT 9600	CTAATTT CTAATTT CTAATTT TCGTGTT TCGTGTT TCGTGTT AGCAAAC		10321 CATTTTAAATTCTTATTCACCTCTGGCAAACCATTCACAAACCATGGTAGTAAGAGAA

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AIGTTATTTCAAGTACTACAGCTGCTTCTAATCTTAGTTGACAGTGATTTTGCCCTGTAG 1440
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                                                 /note= "No. 6228594mal or wild-type (unaffected)
Hereditary Hemochromatosis (HH) gene
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24d1(G)
    5606..5881
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allele
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                                                                                                                                                                                                       NAME/KEY: -
LOCATION: 3852..3891
COTHER INFORMATION: /note= "start and stop positions:
OTHER INFORMATION: normal or wild-type (unaffected);
OTHER INFORMATION: sequence surrounding variant for OTHER INFORMATION: allele (SEQ ID NO:41)"
                                                                                                                                                                                                                                                                                                        NAME/KEY: -
NAME/KEY: -
LOCATION: 5507..6023
LOCATION: 5507..6023
OTHER INFORMATION: /note- "start and stop positions
OTHER INFORMATION: normal or wild-type (unaffected)
OTHER INFORMATION: sequence surrounding variant for
OTHER INFORMATION: allele (SEQ ID NO:20)"
NAME/KEY: allele
                                                                                                   FEATURE:
NAME/KEY: -
COCATION: 140..7319
OTHER INFORMATION: /note= "start and stop positions of ther information: normal or wild-type (unaffected): OTHER INFORMATION: cDNA (SEQ ID NO:9)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /phenotype= "normal or wild-type
(unaffected)"
/label= 24d1
                                                                                                                                                                                                                                                                                                                                                                                                                                            or wild-type
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LOCATION: join(361..436, 3762..4025, 4235..4510, LOCATION: 6040..6153, 7107..7147)

OTHER INFORMATION: /product= "Hereditary Hemochron OTHER INFORMATION: /note= "No. 6228594mal or wild OTHER INFORMATION: Hereditary Hemochromatosis (HH OTHER INFORMATION: allele"
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); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 10823;
                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: replace(3872, "c")
OTHER INFORMATION: /phenctype= "normal
OTHER INFORMATION: (unaffected)"
OTHER INFORMATION: /label= 2442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "normal
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(unaffected)"
/label= 24d7
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LOCATION: replace(5834, "q")
OTHER INFORMATION: /phenotype
OTHER INFORMATION: (unaffected
OTHER INFORMATION: /label= 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: replace(3878, "a")
OTHER INFORMATION: (unaffecte
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Best Local Similarity 100.0
Matches 10823; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: allele
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2640 2700 2760 2760 2820 2880 2880 2940 2940 3000 3060 3060 3120 3120 3180 3180 3240 3300 3300 3360 3360 3420 3480 3480 3540 3540 3600 3600 2580 2700 3420 GITCAAGACCAGCCTGGGCAACACAGCAAAAAACCCCTTCTCTACAAAAAATACAAAAATA TATATTCTGAAGGAAGTTGCTGAAGGATTCTATGTTGTGTGAGAGAAAGAGAAATTGG GTTCAAGACCAGCCTGGGCAACACAGCAAAACCCCTTCTTCTACAAAAATACAAAAATTA GCTGGGTGTGGTGCATGCACCTGTGATCCTAGCTACTCGGGAGGCTGAGGTGGAGGCTA TTGCTTGAGCCCAGGAAGTTGAGGCTGCAGTGAGCCATGACTGTGCCACTGTACTTCAGC CTAGGTGACAGAGCAAGACCCTGTCTCCCCTGACCCCCTGAAAAAGAGAAGAGTTAAAGT CTAGGTGACAGAGCAAGACCCTGTCTCCCCTGACCCCTGAAAAGAGAAGAAGTTAAAGT TGACTTTGTTCTTTATTTAATTTTTATTGGCCTGAGCAGTGGGGTAATTGGCAATGCCAT CAGTGTAAGAATTCAGGACCAAGGCTGGGCACGGTGGCTCACTTCTGTAATCCCAGCACT TTGGTGGCTGAGGCAGGTAGATCATTTGAGGTCAGGAGTTTGAGACAAGCTTGGCCAACA TGGTGAAACCCCCATGTCTACTAAAATACAAAATTAGCCTGGTGTGGTGGCGCACGCCT CTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAACTGAAGGAATTATTCCTCAGGATTTGGG CTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAACTGAAGGAATTATTCCTCAGGATTTGGG TCTAATTTGCCCTGAGCACCAACTCCTGAGTTCAACTACCATGGCTAGACACCCTTAAC ATTITCTAGAATCCACCAGCTITAGTGGAGTCTGTCTAATCATGAGTATTGGAATAGGAT CTGGGGGCAGTGAGGGGGTGGCAGCCACGTGTGGCAGAAAAAGCACACAAAGAAGAGC 2521 2581 2701 2941 3001 3061 3301 3541 2641 2641 2701 2761 2761 2821 2821 2881 2881 2941 3001 3061 3121 3121 3181 3181 3241 3241 3301 3361 3421 3541 2521 2581 3361 3421 3481 3481 Op Oy Op Q Dp DP OY DP Dp D Q QY Db δ g δ οy ογ g oy Db oy Db do Oy Ob οχ g οŽ Q οy g Ωy 셤 ò

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ACCCAGGACTGTCATATGGAAGAAGACAGGACTGCAACTCACCCTTCACAAAATGAGGA 	. CCAGACACAGGTGATGGGTATGAGGTGGGGGGTGTGGGGGCCTCAACATCCTGCTCCC	CTCCTACTACACATGGTTAAGGCCTGTTGCTCTGTCTCCAGGTTCACACTCTCTGCACTA	CCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCTTGTTTGAAGCTTTGGGGTA	CGTGGATGACCAGCTGTTCGTGTTCTATGATNATGAGAGTCGCCGTGTGGAGCCCCGAAC	TCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGCAGCTGAGTCAGAGTCTGAA	AGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTATGGAAAATCACACACGGIIIIIIIIII	CAAGGTAIGIGGAGAGGGGCCTCACCTTCCTGAGGTIGTCAGAGCTTTTCATCTTTTC	ATGCATCTTGAAGGAAACAGCTGGAAGTCTGAGGTCTTGTGGGAGCAGGGAAGAGGAAG 	GAATTTGCTTCCTGAGATCATTTGGTCCTTGGGGATGGTGGAAATAGGGACCTATTCCTT 	TGGTTGCAGTTAACAAGGCTGGGGATTTTTCCAGAGTCCCACACCCTGCAGGTCATCGTG	GGCTGTGAAATGCAAGAAGAACAACAGTACCGAGGGCTACTGGAAGTACGGGTATGATGGG 	CAGGACCACCTTGAATTCTGCCCTGACACTGGATTGGAGAGCAGCAGAACCCAGGGCC 	TGGCCCACCAAGCTGGAGTGGGAAAGGCACAAGATTCGGGCCAGGAGAACAGGGCCTAC 	CTGGAGAGGGACTGCCCTGCACAGCTGCAGTTGCTGGAGCTGGGGAGAGGTGTTTTG 	GACCAACAAGGTAIGGIGGAAACACACTICIGCCCCTAIACICTGIAGIGGCAGAGIGGAGG 	AGGTTGCAGGGACGGGATCCCTGGTTGCAGTTTCAGAGGTGGCTGAGGCTGTGTGCCTC	TCCAAATTCTGGGAAGGGACTTTCTCAATCCTAGAGTCTCTACCTTATAATTGAGATGTA	TGAGACAGCCACAAGTCATGGGTTTAATTTCTTTTTCTCCATGCATATGGCTCAAAGGGAA
3601	3661	3721	3781 3781	3841	3901 3901	3961 3961	4021	4081	4141	4201	4261	4321	4381	4441	4501	4561	4621	4681
άy Db	Qy Db	Oy Db	Q Q	QY Db	QY Db	Qy Db	Qy Db	Q Dp	Qy Db	Qy	Oy Op	Oy Dp	oy Op	O.Y Db	Qy Dp	Qy Db	Qy Db	QY

4740 4800 4980 5040 5040 5100 5100 5160 5160 5220 5220 5280 5280 5340 5640 5400 5400 5460 5460 5520 5580 5580 5700 5700 5760 5760 5820 GTGTCTATGGCCCTTGCTTTTATTTAACCAATAATCTTTTGTATATTTATACCTGTTAA ACCCGTCTCTAAAAAATACAAAATTAGCTGGTCACAGTCATGCGCACCTGTAGTCCCA GCTAATTGGAAGGCTGAGGCAGGAGCATCGCTTGAACCTGGGAAGCGGAAGTTGCACTGA GCCAAGATCGCGCCACTGCACTCCAGCCTAGGCAGCAGAGTGAGACTCCATCTTAAAAAA AAAAAAAAAAAAAAAAAAAGAGAATTCAGAGATCTCAGCTATCATATGAATACCAGGACAAA AGAACATAGCAATAATCACTGAAGCTACCTATCTTACAAGTCCGCTTCTTATAACAATGC CCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCCCCTGGGGGAAGAG AAATTCAGAAATGTCAAGGCCGGGCACGGTGGCTCACCCCTGTAATCCCAGCACTTTGGG CTCCTAGGTTGACCCAGGTGAACTGACCATCTGTATTCAATCATTTCAATGCACATAA AGGGCAATTTTATCTATCAGAACAAGAACATGGGTAACAGATATGTATTTACATGTG AGGAGAACAAGCTGATCTGACTGCTCTCCAAGTGACACTGTGTTAGAGTCCAATCTTAGG TCTTCAGTGACCACTCTACGGTGTCGGGCCTTGAACTACTACCCCCAGAACATCACCATG AAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCTAAAGACGTATTG AACCTATAGAAGGAAGTGAAAGTTCCAGTCTTCCTGGCAAGGGTAAACAGATCCCCTCTC CTCATCCTTCCTCTTTCCTGTCAAGTGCCTCCTTTGGTGAAGGTGACACATCATGTGACC 4741 4681 4741 4801 4861 4861 4801 4921 4921 5041 5101 5341 5401 4981 4981 5041 5101 5161 5221 5281 5281 5401 5461 5461 5521 5521 5581 5581 5641 5641 5701 5701 5761 ď ΣХ q ζ g ζ q Σ q ζ q ζ q 2 g Š ð ₹ · 6 ₹ ą ζ g ⋩ ą ζ 9 $\stackrel{\sim}{2}$ ą ⋩ ð ⋩ ð ζ á ζ

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	19/6	5821	5881	5941	6001	6061	6121	6181 6181	6241	6301	6361	6421	6481	6541	6601	6661	6721 6721	6781 6781	6841
Ċ	Q C	oy O	Oy Db	Qy Dp	Oy Dp	Oy Dp	Oy Db	Qy	Oy Dp	oy Og	Oy Dp	Qy Dp	Qy Db	Oy Dp	Qy Db	Oy Db	Qy Db	Oy DD	oy Ob

ACATACACCTATGTCATTTCATTTTGGAACAGGACTCCTTAAATTTGGGGGAACAGGACTCCTTAAATTTGGGGGAACAGGACTCCTTAAATTTGGGGGAACACATTTTTGGAAGAGACTCCTTAAATTTGGGGGA AGGTGTCATACAGATTTGCAAAGTTTAATGGTGCCTTCATTTGGGATGCTACTCAGTAT TCTCTCATGAACCTCAAGCTGCATCTAGAGGCTTCCTTCATTTCCTCCGTCACCTCAGAG TTCCAGATGAGAGATAATGGTTCTTGAAATCCAATAGTGCCCAGGTCTAAATTGAGATGG GTGAATGAGGAAAATAAGGAAGAAGAAGAGGCAAGATGGTGCCTAGGTTTGTGATGCCT CTITCCTGGGTCTCTTGTCTCCACAGGAGGAGCCATGGGGCCACTACGTCTTAGCTGAACG TGAGTGACACGCAGCCTGCAGACTCACTGTGGGAAGGAGACAAAAACTAGAGACTCAAAGA qq QQ g Op ōλ QQ g Ωp Ob Qy Db QY οy Ω Qγ Oy Oy Oy Ob QΥ q δ δ qq ΟŻ ٥y g g 99 99 Ω δy

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g q	7981	ALTATION TO THE TOTAL TACTICAL TOTAL	
Qy Dp	8041	CATGCATTACTGCATGCACTTCTACAATAATTCTATGAGATAGGTACTATTATCCCCAT 8100 	
Qy Db	8101	GTAATCCC 816	
Qy Db	8161 8161	AGCACTTTGGGAGGCCAAAGCGGGTGGATCACGAGGTCAGGAGATCGAGACCATCCTGGC 8220 	
Oy Db	8221	ATAAAAATACAAAAATTAGCTGGGCGTGGTGGCG 828 	
Qy	8281 8281	GGAGG 834 GGAGG 834	
Qy Dp	8341	CAGAGCTTGCAGTGAGCGGAGTTTGCGCCACTGCACTCCAGCCTAGGTGACAGAGTGAGA 8400 	
Qy Db	8401	CTCCATCTCAAAAAAATAAAAATAAAAATAAAAAATGAAAAAAAA	
Qy Dp	8461	TAGAGTATCTCATAGTTTGTCAGTGATAGAAACAGGTTTCAAACTCAGTCAATCTGACCG 8520 	
Qy Dp	8521 8521	TITGATACATCTCAGACACCACTACATTCAGTAGTTTAGATGCCTAGAATAAATA	
Qy	8581 8581	GGAAGGAGATGGCTCTTCTCTTGTCTCATTGTGTTTCTTGTGAGTGA	
QY	8641	GAAGGGGAACAGCGAAAACAACCAACTGATCCTGAGCTGTCATGTTTCCTTTAAAAGTC 8700 	
Qy Db	8701 8701	CCTGAAGGAAGGTCCTGGAATGTGACTCCTTGCTCTTGTTGCTCTTTGGCATTCA 8760 	
Qy	8761 8761	TITCITIGGACCCIACGCAAGGACTGIAAITGGIGGGGACAGCIAGTGGCCCTGCTGGGC 8820 	
QY	8821 8821	TTCACACACGGTGTCCTCCTAGGCCAGTGCCTCTGGAGTCAGAACTCTGGTGGTATTTC 8880 	
Qy Dp	8881 8881	CCTCAATGAAGTGGAGTAAGCTCTCTCATTTTGAGATGGTATAATGGAAGCCACCAAGTG 8940 	
O.Y D.b	8941	GCTTAGAGGATGCCCAGGTCCTTCCATGGAGCCACTGGGGTTCCGGTGCACATTAAAAAA 9000 	
QY Db	9001	AAAATCTAACCAGGACATTCAGGAATTGCTAGATTCTGGGAAATCAGTTCACCATGTTCA 9060 	
٥y	9061	GCTGGAGTGCAATGGCATGAT 912	

qq	9061		9120
Qγ	9121	CTCGGCTCACTGTAACCTCTGCCTCCCAGGTTCAAGCGATTCTCCTGTCTCAGCCTCCCA	9180
QO	9121	CGGCTCACTGTAACCTCTGCCTCCCAGGTTCAAGCGATTCTCCTGTCTCAGCCTCC	9180
Qy	9181	ACTAGCTGGGATTACAGGCGTGCACCACCATGCCCGGCTAATTTTTGTATTTTTAGTAGA	9240
δλ	24	GTTGGCCAGGCTGGTCTCGAACTCTCCTGACCTCGTGATCGG	30
QC C	77	LAGGGTTTCACCATGTTGGCCAGGCTGGTCTCGAACTCTCCTGACCTCGTGATCC	9300
Qy	9301	TGCCTCGGCCTCCCAAAGTGCTGAGATTACAGGTGTGAGCCACCCTGCCCAGCCGTCAAA 	9360
Qy	9361	GAGTCTTAATATATATCCAGATGCCATGTGTTTACTTTATGTTACTACATGCACTT	9420
QQ	9361		9420
δy	9421	GCTGCATAAATGTGGTACAAGCATTCTGTCTTGAAGGGCAGGTGCTTCAGGATACCATAT	9480
QQ	9421	CTGCATAAATGTGGTACAAGCATTCTGTCTTGAAGGGCAGGTGCTTCAGGATACCAT	9480
92	9481	ACAGCTCAGAAGTTTCTTTAGGCATTAAATTTTAGCAAAGATATCTATC	7.
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7 d	54	TTAAACCATTTCTTTTTTGTGGTTAGAAAGTTATGTAGAAAAAGTAAAGGTTA	09
ΟY	9601	CGCTCATTGTAGAAAGCTATAAAATGAATACAATTAAAGCTGTTATTTAATTAGCC	0996
qq	9601	GCTCATTGTAGAAAAGCTATAAAATGAATACAATTAAAGCTGTTATTTAATTAGCCCA	0996
0y	9	TGAAAAACTATTAACAACTTGTCTATTACCTGTTAGTATTATTGTTGCATTAAAAATGCA	72
3 ,	9 6	ARCIALIAACAACIIGICIATIACCIGIIAGIATTATTGITGCATTAAAAATGC	7
QY Dp	9721 9721	TATACTITAATAAATGTATATIGTATIGTATACTGCATGATITTATIGAAGTICTIGTIC	9780
ΟŸ	9781	CTTGTGTATATACTTAATCGCTTTGTCATTTTGGAGACATTATTTTGCTTCTAATT	9840
qq	9781	AICTIGIGHTATATACTTAATCGCTTTGTCATTTTGGAGACATTTATTT	9840
δλ	9841	CTTTACATTTTGTCTTACGGAATATTTTCATTCAACTGTGGTAGCCGAATTAATCGTGTT	0066
qq	9841	TTTACATTTTGTCTTACGGAATATTTTCATTCAACTGTGGTAGCCGAATTAATCGTGT	0066
QY	9901	TCTTCACTCTAGGGACATTGTCGTCTAAGTTGTAAGACATTGGTTATTTTACCAGCAAAC	0966
qq	9901	CTTCACTCTAGGGACATTGTCGTCTAAGTTGTAAGACATTGGTTATTTTACCAGCAAA	0966
QY	9961	CATTCTGAAAGCATATGACAAATTATTTCTCTCTTAATATCTTACTATACTGAAAGCAGA	10020
qq	9961	attetgaaagcatatgacaaattattetetetaatatettactataegaageag	10020
Qγ	10021	CTGCTATAAGGCTTCACTTACTCTACCTCATAAGGAATATGTTACAATTAATT	10080
qq	10021	SCIATAAGGCTTCACTTACTCTTCTACCTCATAAGGAATATGTTACAATTAATT	10080
QY	10081	AGGTAAGCATTTGTTTTATATTGGTTTTATTTCACCTGGGCTGAGATTTCAAGAAACACC	10140
QY	10141	CACATTTCACTAACACATTTACTAAACATCAGCAACTGTGG	10200

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CDS
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LOCATION:
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Matches 10823;
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10141 CCAGTCTTCACAGTAACACATTTCACTAACACATTTACTAAACATCAGCAACTGTGGCCT 10200
                                            CATITIAAATICTTATICACCICIGGCAAAACCATICACAAACCAIGGIAGIAAAGAGAA 10380
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APPLICANT: Thomas, Winston J.

APPLICANT: Feder, John N.

APPLICANT: GILKE, Andreas

APPLICANT: Ruddy, David

APPLICANT: Tsuchihashi, Zenta

APPLICANT: Tsuchihashi, Zenta

APPLICANT: Horolif, Roger K.

TILE OF INVENTION: Hereditary Hemochromatosis Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect Version
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ADDRESSEE: Pennie &
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AMATION: /product= "Hereditary Hemochromatosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /phenotype= "Hereditary Hemochromatosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Hereditary Hemochromatosis (HH) gene 24d1 allele"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: -
LOCATION: 140..7319
COTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: 24d1 allele cDNA (SEQ ID NO:10)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "start and stop positions for
genomic sequence surrounding variant
for 24d2(C) allele (SEQ ID NO:41)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "start and stop positions for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genomic sequence surrounding variant for 24d1(A) allele (SEQ ID NO:21)"
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larity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                   8907-0088-999
CURRENT APPLICATION DATA: US/09/503,444A
                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/652,265
FILING DATE: 23-May-1996
PRIOR APPLICATION NATA:
APPLICATION NUMBER: 08/632,673
FILING DATE: 16-Apr-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/630,912
FILING DATE: 04-Apr-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= 24d1
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OTHER INFORMATION: /phenotype
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                           NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/POCKET NUMBER: 890'
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-90-9090
TELEFAX: 212-869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mutation"
                                                                                                                                                                                                                                                                                                              28,462
                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 10825 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                              14-Feb-2000
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OTHER INFORMATION: /r
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FEATURE:
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OTHER INFORMATION:
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                             APPLICATION NUMBER:
FILING DATE: 14-Fe
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	18	240	300	360	420		540	009	099	720	780	840	006	096	1020	1080	1140	1200
AATATCTAAAAGTTCAGATCAGAACATTGCGAAGCTACTTTCCCCAATCAACAACACCCC TCAGGATTTAAAAACCAAGGGGGACACTTGGATCACCTAGTTTTTCAAAAAACAAAGGAACAAAGAAAAAAAA		. CTGCTGTAGGAGAGAGAACTAAAGTTCTGAAAGACCTGTTGCTTTTCACCAGGAAGTT 	. TTACTGGGCATCTCCTGAGCCTAGGCAATAGCTGTAGGGTGACTTCTGGAGCCATCCCGGGTGALIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	TITCCCGGCCCCCCAAAAGAAGCGGAGAIITAAACGGGGACGIGCGGCCAGAGCIGGGGAA 	ATGGGCCCGCGAGCCAGGCGGCGCTCTCCTCTGATGCTTTTGCAGACCGCGGTCCTG	CAGGGGCCTTGCTGCGTGAGTCCGAGGGCTGCGGGGGAACTAGGGGGGGG	GAAAAATCGAAACTAGCTTTTTCTTTGCGCTTGGGAGTTTGCTAACTTTGGAGGACCTGC 	TCAACCCTATCCGCAAGCCCCTCTCCCTACTTTCTGCGTCCAGACCCGTGAGGGAGTGC 	CTACCACTGAACTGCAGATAGGGGTCCCTCGCCCCAGGACCTGCCCCCTCCCCGGGCTGT	CCCGGCTCTGCGGAGTGACTTTTGGAACCGCCCACTCCCTTCCCCCAACTAGATGCTTT	TAAATAAATCTCGTAGTTCCTCACTTGAGCTGAGCTAAGCCTGGGGCTCCTTGAACCTGG	AACTCGGGTTTATTTCCAATGTCAGCTGTGCAGTTTTTTCCCCAGTCATCTCCAAACAGG	AAGTTCTTCCCTGAGTGCTTGCCGAGAAGGCTGAGCAAACCCACAGCAGGATCCGCACGG	GGTTTCCACCTCAGAACGAATGCGTTGGGCGGTGGGGGCGCGAAAGAGTGGCGTTGGGGA 	TCTGAATTCTTCACCATTCCACCACTFTTGGTGAGACCTGGGGTGGAGGTCTCTAGGTT 	GGGAGGCTCCTGAGAGAGGCCTACCTCGGGCCTTTCCCCACTCTTGGCAATTGTTCTTTT 	GCCTGGAAAATTAAGTATATGTTAGTTTTGAACGTTTGAACTGAACAATTCTCTTTTCGG	CTAGGCTTTATTGATTTGCAATGTGCTGTAATTAAGAGGCCTCTCTTACAAGTACTGA
61	(7)	181	241	301	361	421	481	541	601	661	721	781	841	901	961	1021	1081	1141
dd Oy	g Q	Qy Db	Qy Dp	Qy Db	QY Db	QY	Qy	Qy	Qy Dp	Qy Db	QY Dp	Oy Dp	Oy Dp	Oy Db	oy Dp	Qy Dp	Qy Db	Qy

Qy do	1201 T	AATGAACATGTAAGCAATGCACTCACTTCTAAGTTACATTCATATCTGATCTTATTGA 126	09
Qy	61 T	TTTCACTAGGCATAGGGGGGGTAGGAGCTAATAATACGTTTATACTAGAAGTTAAATA	0 0
QQ	61 T		20
QY	1321 GC	ATAACTCTTTCAGGTTACAAAGAACATAAATAATCTGGTTTTCTG	80
Q	1321 GC	TCAGATTATATAACTCTTTTCAGGTTACAAAGAACATAAATAA	80
Qy	1381 AT	STTATTTCAAGTACTACAGCTGCTTCTAATCTTAGTTGACAGTGATTTTGCCCTGTAG 1	40
qq	1381 A	GTTATTICAAGTACTACAGCTGCTTCTAATCTTAGTTGACAGTGATTTTGCCCTGTAG 1	440
ΟŊ	41 1	CTGTGGGTCACACGCCGCCTCAGCACAGCACTTTGAGTTTTGGTA 1	00
qq	1441 TC	ACAGTGTTCTGTGGGTCACACGCCGCCTCAGCACACGCACTTTGAGTTTTGGT	
δy		3TGTATCCACATTTACACATGACAAGAATGAGGCATGGCACGGCCTGCTTG	
qq	1501 CI	CTACGTGTATCCACATTTTACACATGACAAGAATGAGGCATGGCACGGCCTGCTTCCTGG 156	
Qy	1561 CZ	16	20
Db	1561 CP	561 CAAATTTATTCAATGGTACACTGGGCTTTGGTGGCAGAGCTCATGTCTCCCACTTCATAGC 162	20
ΟŊ	1621 TP		80
QQ	1621 TP	, ,	80
Qy	1681 AA	1-1	40
QQ	1681 AA	-	40
δλ	1741 CA		00
qq	1741 CA	-	00
QY	1801 GA		09
qq	1801 GA	_	09
δŏ	1861 GA	192	50
qq	1861 GA	192	20
QY	1921 AA	198	80
Dp	1921 AA	198	80
δλ	1981 TT	204	0
qq	1981 TT	204	0
δý	2041 CG	210	00
qq	2041 CG	210	8
Qy	2101 CCT	216	90
qq	2101 cc	CCTACTCACTAGGTGCTAGGAGCACTCCCCCAGTCTTGACAACCAAAAATGTCTCT 216	20
Qy	2161 AAA	CTTTGCCACATGTCACCTAGTAGACAAACTCCTGGTTAAGAAGCTCGGGTTGAAAAA 222	20
Ор	2161 AA	DITIGCCACAIGICACCIAGIAGACAAACICCIGGIIAAGAAGCICGGGIIGAAAA 222	02
δy	2221 AAT	AAACAAGTAGTGCTGGGGAGTAGAGGCCAAGAAGTAGGTAATGGGCTCAGAAGAGA 228	00
QQ	2221 AA	AAACAAGTAGTGGGGGAGTAGAGGCCAAGAGT	00

2340 2340 2400 2400 2460	52	2580	2640	2700	2760 2760	2820 2820	2880 2880	2940 2940	3000	3060	3120	3180 3180	3240	3300	3360	3420
	GGGGCACAGTAAAAGCAGGGGGCCCCAGCCAGGAAGCTG11AAAAGGTCAGGCAAGA FAGTGGAGTGGGCTGGGTGGGAACAGAAAAGGGGGTGACAAACCATTGTCTCCTGA 	TATATTCTGAAGGAAGTTGCTGAAGGATTCTATGTTGTGTGAGAGAAAGAGAAATTGG 	CIGGGIGTAGTAGCICATGCCAAGGAGGCCAAGGACAGCAGATTCCTGAGCTCAGGA 	GTTCAAGACCAGCCTGGGCAACACAGCAAAACCCCTTCTCTACAAAAATACAAAATTA 	GCTGGGTGTGGTGGCATGCACCTGTGATCCTAGCTACTCGGGAGGCTGAGGTGGAGGTAALT	TIGCTIGAGCCCAGGAAGTIGAGGCTGCAGTGAGCCATGACTGTGCCACTGTACTTCAGC	CTAGGTGACAGAGCAAGACCTGTCTCCCTGACCCCCTGAAAAGAGAAGAGTTAAAGT	TGACTTTGTTCTTTATTTTAATTTTATTGGCCTGAGCAGTGGGGTAATTGGCAATGCCAT	TTCTGAGATGGTGAAGGCAGAGGGAAAGAGCAGTTTGGGGTAAATCAAGGATCTGCATTTG	GGACATGTTAAGTTTGAGATTCCAGTCAGCTTCCAAGTGGTGAGGCCACATAGGCAGTT 	. CAGTGTAAGAATTCAGGACCAAGGCTGGGCACGGTGGCTCACTTCTGTAATCCCAGCACT 	TTGGTGGCTGAGGCAGGTAGATCATTGAGGTCAGGAGTTTGAGACAAGCTTGGCCAACA	1 TGGTGAAACCCCATGTCTACTAAAATACAAAAATTAGCCTGGTGTGGTGGGGGGCACCT	ATAGTCCCAGGTTTTCAGGAGGCTTAGGTAGGAGATCCCTTGAACCCAGGAGGTGCAGG	1 TTGCAGTGAGCTGAGATTGTGCCACTGCAGTCCAGCCTGGGTGATAGAGTGAGACTCTGT	CTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAACTGAAGGAATTATTCCTCAGGATTTGGG
28 28 34 40	2461 2461 2461	2521 2521	2581 2581	2641	2701	2761 2761	2821	2881 2881	2941	3001	3061	3121	3181	3241	3301	3361
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4140 4440 4440 4080 4080 4140 4200 4200 4260 4260 4320 4320 4380 4380 4500 4020 CCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCTTGTAGAGCTTTGGGCTA 3840 3900 3420 3480 3600 3660 3660 3720 3720 3780 3780 CTGGAQAGGGACTGCCCTGCACCTGCAGCAGTTGCTGGAGCTGGGGAGAGAGTGTTTG ATGCATCTTGAAGGAAACAGCTGGAAGTCTGAGGTCTTGTGGGAGCAGGGAAGAGGAAGAGAAGAGTCTTGTGGGAAGAGCAGGGAAGAGAAGAAGAAGAGTCTTGTGGGGAGCAGGGAAGAAGAAGAGTCTGAGGTCTTGTGGGGAGCAGGGAAGAAGAGGGAAGAAGAGTCTTGTGGGGAGCAGGGAAGAAGAGGGAAGA GGCTGTGAAATGCAAGAAGACAACAGTACCGAGGGCTACTGGAAGTACGGGTATGATGG CTCCTACTACACATGGTTAAGGCCTGTTGCTCTGTCTCCAGGTTCACACTCTCTGCACTA CGTGGATGACCAGCTGTTCGTGTTCTATGATNATGAGAGTCGCCGTGTGGAGCCCCGAAC TCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGCAGCTGAGTCAGAGTCTGAA AGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTATGGAAAATCACAACCACAG GAATTTGCTTCCTGAGATCATTTGGTCCTTGGGGATGGTGGAAATAGGGACCTATTCCTT TGGTTGCAGTTAACAAGGCTGGGGATTTTTCCAGAGTCCCACACCCTGCAGGTCATCCTG CCAGACACAGCTGATGGTATGAGTTGATGCAGGTGTGTGGAGCCTCAACATCCTGCTCCC CAAGGGTATGTGGAGAGGGGGCCTCACCTTCCTGAGGTTGTCAGAGCTTTTCATCTTTTC ATTITICIAGAATCCACCAGCTTTAGTGGAGTCTGTCTAATCATGAGTATTGGAATAGGAT ACCCAGGACTGTCATATGGAAGAAGACAGGACTGCAACTCACCTTCACAAAATGAGGA TCTAATTTGCCCTGAGCACCAACTCCTGAGTTCAACTACCATGGCTAGACACACCTTAAC 3961 4081 4141 4141 4201 4261 4261 4321 4441 4021 4021 4081 4201 4321 3841 3901 3961 3421 3481 3541 3541 3601 3601 3661 3721 3781 3781 3841 3901 3361 3481 3661 3721 3421 Ω g ŏ QQ g pp δ g ò Db Op δλ g οy g οχ g δ qq Qγ q Ω QQ QY ò Ω QΥ Db Q Dp δλ δ g Qγ οy QΫ

qq	4441	CTGGAGAGGGACTGCCCTGCACAGCTGCAGGTTGCTGGAGCTGGGGAGGTGTTTTG 4500		
ΟŊ	4501	CTCTAGTGGCAGAGTGGAG	ΟŊ	226
QQ	4501	ق ا	Dp	558
ò	4561	.C9V	QY	264
원	56	62	đ	264
Qy	4621	CCAAATTCTGGGAAGGGACTTTCTCAATCCTAGAGTCTCTACCTTATAATTGAGATGTA 468	QY	57(
QQ	4621	68	Q Q	~
δy	4681	GAGACAGCCACAAGTCATGGGTTTAATTTCTTTTTTCTCCATGCATATG	ΟŊ	576
qq	4681	7	qq	
Qy	4741	480	QY	283
qq	4741		qo ,	
ΟŊ	4801	AAATTCAGAAATGTCAAGGCCGGCCACGGTGGCTCACCCCTGTAATCCCAGCACTTTGGG 4860	Š d	280
qq	4801	AAATTCAGAAATGTCAAGGCCGGGCACGGTGGCTCACCCTGTAATCCCAGCACTTTGGG 4860	9 3	28.0
Ολ	4861		ž f	594
qq	4861	AGGCCGAGGCGGGTGGTCACAAGGTCAGGAGTTTGAGACCAGCCTGACCAACATGGTGAA 4920		
žo ž	4921	86	do Dp	009
3 8	1264	4 4 9 8	Qy	909
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οy	5041	A 510	Qy	612
g	5041		qq	612
δò	5101	ŗ.	Qy	618
ු යු	5101		QQ	618
δý	5161	ATATCAAGTGAGGCCACTTATCAGAGTAGAAGAATCCTTTAGGTTAAAAGTTTCTTTC	δy	624
q	5161		qq	624
δy	5221	AGAACATAGCAATAATCACTGAAGCTACCTATCTTACAAGTCCGCTTCTTATAACAATGC 5280	δλ	63(
qq	5221	28	qq	63(
ΩŸ	5281	CICCTAGGITGACCCCAGGIGAAACTGACCATCTGTATTCAATCATTTCAATGCACATAA 5340	δy	636
QC	5281	34	qq	636
δy	5341	TTATCTATCAGAACAAGAACATGGGTAACAGATATGTATATTTACATGTG 540	QY	642
g	5341	4	qq	642
δλ	5401	AGCTGATCTGACTGCTCTCCAAGTGACACTGTGTTAGAGTCCAATCTTAGG 546	Qy	648
qq	5401		QQ	648
δý	5461	ACACAAAATGGTGTCTCCTGTAGCTTGTTTTTTTTCTGAAAAGGGTATTTCCTTCC	Qy	654
q	5461	52	QΩ	654
ΟŊ	5521	AACCTATAGAAGGAAGTGAAAGTTCCAGTCTTCCTGGCAAGGGTAAACAGATCCCCTCTC 5580	ΟŊ	99
qq	5521	28	Op	999

TCTTCAGTGACCACTCTACGGTGTCGGGCCTTGAACTACCCCCAGAACATCACCATG AAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCTAAAGACGTATTG TCTCAGAACCCAAATCTGGTAGGGAATGAAATTGATAGCAAGTAAATGTAGTTAAAGAAG ATCACATTCAGCTGGGGATCAAGATAGCCTTCTGGATCTTGAAGGAGAAGCTGGATTCCA CTCATCCTTCCTCTTTCCTGTCAAGTGCCTCCTTTGGTGAAGGTGACACATCATGTGACC TGAGGAGGTAATTATGGCAGTGAGATGAGGATCTGCTCTTTGTTAGGGGGTGGGCTGAGG GIGGCAATCAAAGGCTTTAACTTGCTTTTTCTGTTTTAGAGCCCTCACCGTCTGGCACCC TAGTCATTGGAGTCATCAGTGGAATTGCTGTTTTTTGTCGTCATCGTTCATTGGAATTT TGTTCATAATATTAAGGAAGAGGCAGGGTTCAAGTGAGTAGGAACAAGGGGGAAGTCTCT AATGGTTCTCCCCAGAATGAAAGTCTCTAATTCAACAACATCTTCAGAGCACCTAATA TITGCAAGAGCTGTTTAAGGTAGTACAGGGGCTTTGAGGTTGAGAAGTCACTGTGGCTAT 0.1

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GAGTATAAGGCATACTGGGGGATTAGAAATTACTGTACCTTAACCCTGAGTTTGCGT 67	AGCTATCACTCACCAATTATGCATTTCTACCCCCTGAACATCTGTGGTGTAGGGAAAAGA 67	GAATCAGAAAGAAGCCAGCTCATACAGAGTCCAAGGGTCTTTTGGGATATTGGGTTATGA 68	TCACTGGGGTGTCATTGAAGGATCCTAAGAAAGGAGGACCACGATCTCCCTTATATGGTG 69	AATGTGTTGTTAAGAAGTTAGATGAGAGGTGAGGAGCACAGTTAGAAAGCCAATAAGCAT 69	TTCCAGATGAGAGATAATGGTTCTTGAAATCCAATAGTGCCCAGGTCTAAATTGAGATGG 70	GTGAATGAGGAAAATAAGGAAGAGAAGAGGCAAGATGGTGCCTAGGTTTGTGATGCTGT GC 11	CTTTCCTGGGTCTCTTGTCTCCACAGGAGCCATGGGGCACTACGTCTTAGCTGAACG 71	TGAGTGACACGCAGCCTGCAGACTCACTGTGGGAAGGAGACAAAACTAGAGACTCAAAGA 72 	GGGAGTGCATTTATGACTCTTCATGTTTCAGGAGAGAGTTGAACCTAAACATAGAAATT 72 	GCCIGACGAACTCCTTGATTTTAGCCTTCTCTGTTCATTTCCTCAAAAGATTTCCCCAT 73 	TTAGGTTTCTGAGTTCCTGCATGCCGGTGATCCCTAGCTGTGACCTCTCCCCTGGAACTG 73	TCTCTCATGAACCTCAAGCTGCATCTAGAGGCTTCCTTCATTTCCTCCGTCACCTCAGAG 74	ACATACACCTATGTCATTTCCTATTTTGGAAGAGGACTCCTTAAATTTGGGGGA 75	CTTACATGATTCATTTAACATCTGAGAAAGCTTTGAACCCTGGGACGTGGCTAGTCAT 75	AACCTJACCAGATTTTTACACATGTATCTATGCATTTTCTGGACCCGTTCAACTTTTCCT 76	TTGAATCCTCTCTCTGTGTTACCCAGTAACTCATCTGTCACCAAGCCTTGGGGATTCTTC 76	CATCTGATTGTGATGTGAGTTGCACAGCTATGAAGGCTGTACACTGCACGAATGGAAGAG 77	GCACCTGTCCCAGAAAAAGCATCATGGCTATCTGTGGGTAGTATGATGGGTGTTTTTAGC 78
6661	6721 6721	6781 6781	6841 6841	6901	6961 6961	7021	7081	7141	7201	7261	7321	7381	7441	7501	7561 7561	7621 7621	7681	7741
Qy	Qy Db	Qy Db	Qy Dp	Oy Dp	Oy Dp	Qy Db	Qy Db	Oy Dp	Qy Db	Oy Dp	Oy Db	Qy	Qy Db	Qy Db	Oy Db	Oy Db	χρος	δŏ

7980 7980 8040 8040 8100 8100 8160 8160 8220 8220 8280 8280 8340 8340 8400 8400 8460 8460 8520 8520 8580 8580 8640 8640 8700 8700 8760 8760 8820 8820 8880 GAAGGGGAACAGCAGAAAACAACCAACTGATCCTCAGCTGTCATGTTTCCTTTAAAAGTC CCTGAAGGAAGGTCCTGGAATGTGACTCCCTTGCTCCTCTGTTGCTCTTTGGCATTCA TTCACACACGGTGTCCTCCCTAGGCCAGTGCCTCTGGAGTCAGAACTCTGGTGGTATTTC ATTATGATAAGGATGATAAAAGCACTTACTTCGTGTCCGACTCTTCTGAGCACCTACTTA CATGCATTACTGCATTCTTACAATAATTCTATGAGATAGGTACTATTATCCCCAT TTCTTTTTTAAATGAAGAAAGTGAAGTAGGCCGGGCACGGTGGCTCACGCCTGTAATCCC ACCCCTGTAGTCCCCAGCTACTCGGAAGGCTGAGGCAGGAGAATGGCATGAACCCAGGAGG CAGAGCTTGCAGTGAGCCGAGTTTGCGCCCACTGCACTCCAGCCTAGGTGACAGAGTGAGA TAGAGTATCTCATAGTTTGTCAGTGATAGAAACAGGTTTCAAACTCAGTCAATCTGACCG TITCITIGGACCCTACGCAAGGACTGTAATIGGTGGGGACAGCTAGTGGCCCTGCTGGGC 7981 8041 8041 8101 8341 8401 8401 8581 8641 8761 7741 7801 7801 7861 7861 7921 7921 7981 8101 8161 8161 8221 8221 8281 8281 8341 8461 8461 8521 8521 8581 8641 8701 8701 8761 8821 Сp g g g QQ qq g q g g οy g οŻ g OD ٥y qq a g qq g QΥ οy ΟY QΥ Qγ Qγ δ Qγ Οy Qγ ò οy Qγ ò ò

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8880	8940 8940	0006	90	12	9180 9180	9240 92 4 0	9300	1360 1360	420	480 480	540 540	009	960	9720 9720	780	840 840	006	096
1 TTCACACACGGTGTCCTCCCTAGGCCAGTGCCTCTGGAGTCAGAACTCTGGTGGTATTTC	1 CCTCAATGAAGTGGAGTAAGCTCTCATTTTGAGATGGTATAATGGAAGCCACCAAGTG	1 GCTTAGAGGATGCCCAGGTCCTTCCATGGAGCCACTGGGGTTCCGGTGCACATTAAAAA (AAAATCTAACCAGGACATTCAGGAATTGCTAGATTCTGGGAAATCAGTTCACCATGTTCA	AAAGAGICITITITITITITITGAGACICIAITGCCCAGGCIGGAGIGCAAIGGCAIGA 	CTCGGCTCACTGTAACCTCTGCCTCCCAGGTTCAAGCGATTCTCCTGTCTCAGCCTCCCCT	AGTAGCTGGGATTACAGGGTGCACCACCATGCCGGCTAATTTTTGTATTTTTGGTAGG	GACAGGGTTTCACCATGTTGGCCAGGCTGGTCTCGAACTCTCCTGACCTCGTGATCGGC	. TGCCTCGGCCTCCCAAAGTGCTGAGATTACAGGTGTGAGCCACCCTGCCCAGCCGTCAAA 9	. AGACTCTTAATATATATATCCAGATGCCATGTGTTTACTTATATGTTACTACATGCACTTG 9	. GCICCATAAATGIGGIACAAGCAITCIGICITGAAGGCCAGGIGCITCAGGAIACCAIAT 9 	. ACACCTCAGAAGTTTCTTCTTTAGGCATTAAATTTTAGCAAAGGATATCTCATCTCTTCTT 9	TTAAACCATTTCTTTTTTTGTGGTTAGAAAGTTATGTAGAAAAAGTAAATGTGATTT 9	ACGCTCATTGTAGAAAAGCTATAAAATGAATACAATTAAAGCTGTTATTTAATTAGCCAG 9 	TGAAAAACTATTAACAACTTGTCTATTACCTGTTAGTATTATTGTTGCATTAAAAATGCA 	TATACTITAATAAATGTATATIGTATIGTATACTGCATGATTITATIGAAGTICTIGTIC 	Arciigretatatacitaatcectitgicatitigeagacatitatigcitctaatit 9 	CTTTACATTTTGTCTTACGGAATATTTTCATTCAACTGTGGGTAGCCGAATTAATCGTGTT 9	TCTTCACTCTAGGGACATTGTCGTCTAAGTTGTAAGACATTGGTTATTTTACCAGCAAAC 9
882	888	894	9001	9061	912	9181	9241	9301	9361 9361	9421	9481	9541	9601	9661	9721	9781 9781	9841	9901
ď	QY Db	QY Db	Ω	Oy Dp	Q P	Qy Db	Oy Db	Qy Db	Qy Db	QQ Dp	Oy Dp	Ογ Db	Qy	Qγ	Oy Db	Qy Db	QY Db	Oy Db

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9961 CATTCTGAAAGCATATGACAAATTATTTCTCTCTTAATATCTTACTATACTGAAAGCAGA 10020
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                                                                                                                                                                     GGGTGACACCTGGTGGCCATAGGTAAATGTACCACGGTGGTCCGGTGACCAGAGATGCAG
                                                                                                                                                           TITITCTGGCTTTATTCATAAATTCTTAAGGTCAACTACATTTGAAAAATCAAAGACCTG
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Patent No. 6228594
GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
APPLICANT: Feder, John N.
APPLICANT: Feder, John N.
APPLICANT: Ruddy, David
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
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LOCATION: join(361..436, 3762..4025, 4235..4510, 5606..5881, LOCATION: join(361..436, 3762..4025, 4235..4510, 5606..5881, LOCATION: 6040..6153, 7107..7147)
COTHER INFORMATION: /product="Hereditary Hemochromatosis other information: mutation"
COTHER INFORMATION: /note="Hereditary Hemochromatosis (HH) other information: gene 24d2 aliele"
FENTURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /phenotype= "Hereditary Hemochromatosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 3852..3891

OTHER INFORMATION: /note= "start and stop positions for

OTHER INFORMATION: genomic sequence surrounding variant

OTHER INFORMATION: for 24d2(G) allele (SEQ ID NO:42)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "start and stop positions for genomic sequence surrounding variant for 24d1(G) allele (SEQ ID NO:20)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: -
LOCATION: 140..7319
COTHER INFORMATION: /note= "start and stop positions
OTHER INFORMATION: 2442 allele cDNA (SEQ ID NO:11)"
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8907-0088-999
                                                                                                                                                                                                                                                                             OPERATING STETEM: WINDOWS >> SOFTWARE: WordPerfect Version 8
CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/503,444A
FILING DATE: 14-Feb-2000
CLASSIFICATION: PROPE APPLICATION NUMBER: 08/652,265
FILING DATE: 23-May-1996
PRIOR APPLICATION NUMBER: 08/632,673
FILING DATE: 16-Apr-1996
PRIOR APPLICATION NUMBER: 08/630,912
FILING DATE: 16-Apr-1996
ATPORNEY APPLICATION NUMBER: 28,462
ATPORNEY APPLICATION NUMBER: 28,462
RECISTRATION NUMBER: 28,462
RELEPROMENIZATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 212-960-9030
                                                                               ME: Pennie & Edmonds LLP
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: allele
LOCATION: replace(3872, "g")
OTHER INFORMATION: /phenotype
                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 6641
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 10825 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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LOCATION: 5507..6023
OTHER INFORMATION: 7no
OTHER INFORMATION: GON
                                                                                                                                                                                  ZIP: 10036
COMPUTER READABLE FORM:
                                                                                                                        CITY: New York
STATE: New York
                                                                                                                                                                   USA
                                                                                    ADDRESSEE:
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                                                                                                        1 TCTAAGGTTGAGATAAAATTTTAAATGTATGATTGAATTTTGAAAATCATAAATATTTA
                                                                                                                                                        61 AATATCTAAAGTTCAGATCAGAACATTGCGAAGCTACTTTCCCCAATCAACAACACCCCT
                                                                                                                                                                                                                                                        181 CTGCTGTAGGAGAGAGAGAACTAAAGTTCTGAAAGACCTGTTGCTTTTCACCAGGAAGTT
                                                                                ó
                                                        Length 10825;
                                                                                 Indels
                                                          DB 4;
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                                                        ; Score 10823; L; Pred. No. 0; 0; Mismatches
           /label= 24d2
                                                        Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 10823; Conservative
OTHER INFORMATION:
OTHER INFORMATION:
   ; OTHER INFO
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US-09-503-444A-5
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GGAGGTCTCTAGGGT 1020	CAAAGTACTGA 120 [rcree 	TTTGAGTTTTGGTA 1500	CTCCACTTCATAGC 1620 	CACTGTTCAAGCCC 1740	AAAATCATGGGTGTTGTGA 1860 	AGTGGGCCTGGCAAG 1980
"IGAATTCTTCACCATTCCACCACTTTGGTGAGACCTGGGGTGGAGGTCTC" [1] 1] 1] 1] 1] 1] 1] 1] 1] 1] 1] 1] 1] 1	SCTTATTGATTTGCAATGGCTGTGTAATTAAGAGGCCTC [1111]	TCAGATTATAACTCTTTCAGGTTACAAAGAACATAAAATTCAGATTACAAAAGTTACAAAATTATATATA		ATTTATTCAATGGTACACTGGCTTTGGTGGCAGAGCTCATGTCTC ATTTATTCAATGGTACACTGGGCTTTGGTGGCAGAGCTCATGTCTC ATTTATTCAATGGTACACTGGGCTTTGGTGGCAGAGCTCATGTCTC GATTCTTAAACATCACACTGCATTAGAGGTTGAATAAAAATTTC	ATTCATTGTTTACAAGTGTAAATGAGTCCCAGCCATGTGTGTG	CAATAAGCAATGAGCAGAAAGATATACAACATCAGG [TAAGAATGATATTGACTGGGAGCAGTATTTCCCAGGCAAACTGAGT [
961 FCFC 171 961 FCFC 1021 GGG3 1021 GGG3 1081 GCCC 1081 GCCC 1081 GCCC	1141 CTAGG 1141 CTAGG 1201 TAATG 1201 TAATG 1201 TAATG	21 G	1441 TGTA(1441 TGTAC 1501 CTACC 1501 CTACC	1561 CAAA 1561 CAAA' 1621 TATGA 	1681 AAA1 1681 AAA1 1741 CAAC 1741 CAAC	1801 GATGP 1801 GATGP 1861 GAAGC 	1921 AAT 1921 AAT 1981 TTG 1981 TTG 2041 CGG
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2580 2940 2100 2160 2160 2220 2280 2280 2340 2340 2400 2400 2460 2460 2520 2520 2580 2640 2640 2700 2700 2760 2760 2820 2820 2880 2880 2940 3000 3000 3060 3060 3120 3120 TTGGTGGCTGAGGCAGGTAGATCATTTGAGGTCAGGAGTTTGAGACAAGCTTGGCCAACA 3180 TTCTGAGATGGTGAAGGCAGAAAAGAGCAGTTTGGGGGTAAATCAAGGATCTGCATTTG GTTCAAGACCAGCCTGGGCAACACAGCAAAAACCCCTTCTCTACAAAAAATACAAAAATAA GTTCAAGACCAGCCTGGGCAACACACAGCAAAACCCCTTCTCTACAAAAATACAAAATTA GCTGGGTGTGGTGCATGCACCTGTGATCCTAGCTACTCGGGAGGCTGAGGTGGAGGGTA TTGCTTGAGCCCAGGAAGTTGAGGCTGCAGTGAGCCATGACTGTGCCACTGTACTTCAGC GCCACAAACAAGGTTGTGCAGGCGCCTGTAGGCTGTGGTGTGAATTCTAGCCAAGGAGTA AAGGGAGCAACAGTAAAAGCAGGGAGCCCAGCCAGGAAGCTGTTACACAGTCCAGGCAAG CTGGGTGTAGTAGCTCATGCCAAGGAGGAGGCCAAGGAGAGCAGATTCCTGAGCACACGA TGACTTTGTTCTTTATTTTAATTTTAATGGCCTGAGCAGTGGGGGTAATTGGCAATGCCAT CAGTGTAAGAATTCAGGACCAAGGCTGGGCACGGTGGCTCACTTCTGTAATCCCAGCACT CCTCCCTACTCACTAGGTGCTAGGAGCACTCCCCCAGTCTTGACAACAAAATGTCTCT AAACTTTGCCACATGTCACCTAGTAGACAAACTCCTGGTTAAGAAGCTCGGGTTGAAAAA AATAAACAAGTAGTGCTGGGGAGTAGAGGCCAAGAAGTAGGTAATGGGCTCAGAAGAGAA ACAGTGATCTGTCACAGGCTTTTAAAAGATTGCTCTGGCTGCTATGTGGAAAGCAGAATG TATATTCTGAAGGAAGTTGCTGAAGGATTCTATGTTGTGTGAGAGAAAAGAAATTGG GGACATGTTAAGTTTGAGATTCCAGTCAGGCTTCCAAGTGGTGAGGCCACATAGGCAGTT 2041 2101 2101 2161 2221 2281 2281 2341 2341 2401 2401 2461 2461 2521 2521 2581 2581 2641 2641 2701 2701 2761 2761 2821 2821 2881 2881 2941 2941 3001 3001 3061 3061 3121 2161 2221 Ω qq Ωp qq Db Op g Dp Qγ QQ δ PP Dp δy οg δy д QQ δy d δ Db qq ΩY Qγ QΥ δ Qγ QΥ QΫ Qγ ď Ω QY δŽ

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. TIGGIGGCIGAGGIAGAICATIIGAGGICAGGAGIIIGAGACAAGCIIGGCCAACA	GGTGAAACCCCATGTCTACTAAAAATACAAAAATTAGCCTGGTGTGGGGGGGG	GGTGAAACCCCATGTCTACTAAAAATACAAAATTAGCCTGGTGTGTGGCGCGCACGC	1 ATAGTCCCAGGTTTTCAGGAGGCTTAGGTAGGAGAATCCCTTGAACCCAGGAGGTGCAGG		1 CTCAAAAAAAAAAAAAAAAAAAAAAAAAAAACTGAAGGAATTATTCCTCAGGATTTGGG 	TCTAATTTGCCCTGAGCACCAACTCCTGAGTTCAACTACCATGGCTAGACACACATAAC	1 ATTTTCTAGAATCCACCAGCTTTAGTGGAGTCTGTCTAATCATGAGTATTGGAATAGGAT 	1 CTGGGGGCAGTGAGGGGTGGCACGTGTGGCAGAGAAAAGCACACAAGAAAGGCAAAGAAGCAAAGAAAGCAAAGAAAGAAAGCAAAGGAAAAGGCAAAGGAAAAGCAAGAGGGGGG	1 ACCCAGGACTGTCATATGGAAGAAAGACAGGACTGCAACTCACCCTTCACAAAATGAGA 	CCAGACACAGCTGATGGTATGAGTTGATGCAGTGTGTGGGAGCCTCAACATCCTGCTCCC	CTCCTACTACACATGGTTAAGGCCTGTTGTTCTGTCTCCAGGTTCACACTCTCTGCACTA	1 CCTCTTCATGGGTGCCTCAGAGCAGCACCATGGTCTTTCCTTGTTTGAAGCTTTGGGCTA 	1 CGTGGATGACCAGCTGTTCGTGTTCTATGATNATGAGAGTCGCCGTGTGGAGCCCCGAAC	1 TCCATGGGTTTCCAGTAGAATTCAAGCCAGATGTGGCTGCAGCTGAGTCAGAGTCTGAA	AGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTATGGAAAATCACAACCACAG	1 CAAGGGTATGTGGAGAGGGGCCTCACCTTCCTGAGGTTGTCAGAGCTTTTCATCTTTTC	1 ATGCATCTTGAAGGAAACAGCTGGAAGTCTGAGGTCTTGTGGGAGCAGCAGGAAGAGGGAAG 	1 GAATTIGCTICCTGAGAICATIGGICCTIGGGGAIGGIGGAAIAGGGACCIATICCIT	1 TGGTTGCAGTTAACAAGGCTGGGGATTTTTCCAGAGTCCCACACCCTGCAGGTCATCTG
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AACATGGGTAACAGATATGTATATTTACATGT	AGGAAGTGAAGGTTGTTTTTTCTGAAAAGGGTATTTCCTTCC	CTTCCTCTTTCCTGTCAGTGCTCTTTTGTTGTTTTTTTTT	CAAGGAGTTCGAACCTAAAGACGTATTI CAACCTTGCTGTACCCCTGGGAAGA IIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	ACCCAGGCCTGGATCAGCCCCTCATTGTG	GGTATGRCTGATGAGAGCCAGGAGCTGAGAAATCTATTGGGGGTTGAGAGGAGTGCC 	TGAGGAGGTAATTATGGCAGTGAGATGAGGATCTGCTCTTTGTTAGGGGGTGGGCTGAGG	GTGGCAATCAAAGGCTTTAACTTGCTTTTCTGTTTTAGAGCCCTCACCGTCTGGCACCC	TAGTCATTGGAGTCATCAGTGGAATTGCTGTTTTTGTCGTCATCTTGTTCATTGGAATTT	TGTTCATAATATTAAGGAAGAGGGGGTTCAAGTGAGTGAG	TAGTACTCTGCCCCAGGGCACAGTGGGAAGAGGGGCAGAGGGGATCTGGCATCCATGGG 	AAGCATTTTCTCATTTATATTCTTTGGGACACCAGCAGCTCCCTGGGAGACAAAAT 	AATGGTTCTCCCCAGAATGAAAGTCTCTAATTCAACAACATCTTCAGAGCACCTACTAT 	TTTGCAAGAGCTGTTTAAGGTACAGGGGCTTTGAGGTTGAGAAGTCACTGTGGGCTAT 	TCTCAGAACCCAAATCTGGTAGGGAATGAAATTGATAGCAAGTAAATGTAATTAAAGAAG
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qq	6421		6480
Qy	6481	CCCCATGAGGTCCTAAAGCAGGCAGGAAGCAAATGCTTAGGGTGTCAAAGG	6540
qq	6481	CCCATGAGGTCCTAAAGCAGGCAGGAAGCAAATGCTTAGGGTGTCAAAGGAAAGAAT	6540
Qy	6541	ATCACATTCAGCTGGGGATCAGATAGCCTTCTGGATCTTGAAGGAGAAGCTGGATTCCA	6600
δλ	6601	3GAGGTCTACACAGACGAGCAACCATGCCAAGTAGG	99
qq	6601	TAGGTGAGGTTGAAGATGATGGGAGGTCTACACAGACGGAGCAACCATGCCAAGTAGG	0999
δy d	6661	GAGTATAAGGCATACTGGGAGATTAGAAATAATTACTGTACCTTAACCCTGAGTTTGCGT	72
3 8	0 0	ASIAIAAGGCAIACIGGGGGGAITAGGAATAATTACTGTACCTTAACCCTGAGTTTGCG	72
do Dp	6721	AGCTATCACTCACCANTATGCATTTCTACCCCCTGAACATCTGTGTGTGGGGAAAAGA 	6780
οy	6781	AATCAGAAAGAAGCCAGCTCATACAGAGTCCAAGGGTCTTTTGGGATATTGGGTTATG	
QQ	6781	TCCAAGGGT	6840
oy i	84	CACTGGGGTGTCATTGAAGATCCTAAGAAAGGAGACCACGATCTCCCTTATATG	0069
QQ	6841	CTGGGGTGTCATTGAAGATCCTAAGAAAGGAGGACCACGATCTCCCTTATATGG	0069
ري م	6901	TGTTAAGAAGTTAGATGAGAGGTGAGGAGACCAGTTAGAAAGCCAATAA POTTTA AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	96
3	5	31611611AGAAGITAGATGAGAGTGAGGAGACAGTTAGAAAGCCAATAAGC	0969
Q Q	6961 6961	TTCCAGATGAGAGATAATGGTTCTTGAAATCCAATACTGCCCAGGTCTAAATTGAGATGG	7020
Qy	7021	GAATGAGGAAAATAAGGAAGAGAGAGAGGCAAGATGGTGCCTAGGTTTGTGATGCCT	00
QQ	7021		7080
δŽ	7081	CTTAGCTGAACG	7140
qq	7081	TTCCTGGGTCTCTTGTCTCCACAGGAGGCGATGGGGGCACTACGTCTTAGCTGAACG	7140
δÿ	7141	SGAGACAAAACTAGAGACTCAAAGA	7200
qq	7141	GAGTGACACGCAGCCTGCAGACTCACTGTGGGGAGGAGACAAAACTAGAGACTCAAAGA	7200
Qy	7201	GGAGTGCATTTATGAGCTCTTCATGTTTCAGGAGAGAGTTGAACCTAAACATAGAAATT	7260
qα	7201	GAGTGCATTTATGAGCTCTTCATGTTTCAGGAGAGAGTTGAAACCTAAACATAGAAATT	7260
Qy	7261	CCAT	7320
Op	7261	CCTGACGAACTCCTTGATTTTAGCCTTCTCTTTTTCTTTTCTTCAAAAAGATTTCCCCAT	7320
δλ	7321	GCTGTGACCTCTCCCCTGGAACTG	7380
qq	7321	AGGTTTCTGAGTTCCTGCAFGCCGGTGATCCCTAGCTGTGTTTTTTTTTT	7380
δλ	7381	CTTCCTTCATTTCCTCCGTCACCTCAGAG	7440
qq	7381	TCTCATGAACCTCAAGCTGCATCTAGAGGCTTCCTTCATTTCCTCCGTCACCTCAGAG	7440
δλ	7441	ACACCTATGTCATTTCCTTATTTTGGAAGAGGCTCCTTAAATTT	7500
ορ	7441	ATACACCTATGTCATTTCATTTCCTATTTTTGGAAGAGGACTCCTTAAATTTGGGG	7500
Qy	7501	CTTACATGATTCATTTTAACATCTGAGAAAGCTTTGAACCCTGGGACGTGGCTAGTCAT 7	7560

7560	7	7680	7740	7800	1 7860	7920	7980	x 8040	r 8100 r 8100	8160 8160 8160	\$ 8220 8220	3 8280 3 8280	3 8340 1 3 8340	A 8400 I A 8400	A 8460 8460	3 8520 8520	A 8580 A 8580	T 8640 8640 8640
CTTACATGATTCATTTTAACATCTGAGAAAAGCTTTGAACCCTGGGACGTGGCTAGTCAI	ACCTTACCAGATTTTACACATGTATCTATGCATTTTCTGGACCCGTTCAACTTTTCTG 	TTGAATCCTCTCTCTGTGTTACCCAGTAACTCATCTGTCACCAAGCCTTGGGGATTCTTC	CATCTGATTGTGATGTGAGTTGCACAGCTATGAAGGCTGTACACTGCACGAATGGAAGGGAGGG	GCACCTGTCCCAGAAAAAGCATCATGGCTATCTGTGGGTAGTATGATGGGTGTTTTTAGC	aggtaggaggcaaatatcttgaaaggggttgtgaagaggtgtttttttt	AGGTGTCATACAGATTTGCAAAGTTTAATGGTGCCTTCATTTGGGATGCTACTCTAGTAT 	TCCAGACCTGAAGAATCACAATAATTTTCTACCTGGTCTCTCCTTGTTCTGATAATGAAA 	ATTATGATAAGGATGATAAAAGCACTTACTTCGTGTCCGACTCTTCTGAGCACCTACTTA	CATGCATTACTGCATGCACTCTTACAATAATTCTATGAGAATAGGTACTATTATCCCCAT	TICTITITTAAAIGAAGAAAGIGAAGITAGCCGGGCACGGTGGCTCACGCCTGTAATCCC 	AGCACTITGGGAGGCCAAAGCGGGTGGATCACGAGGTCAGGAGATCGAGACCATCCTGGC	TAACATGGTGAACCCCATCTCTAATAAAATACAAAAATTAGCTGGGCGTGGTGGGCGG 	ACGCCTGTAGTCCCAGCTACTCGGAAGGCTGAGGCAGGAGAATGGCATGAACCCAGGAGGIIIIIIIIII	CAGAGCTIGCAGTGAGCCGAGTTIGCGCCACTGCACTCCAGCCTAGGTGACAGAGTGAGAGTGACAGAGTGAGAGTGAGAGTGAGCTTTGCAGCTGAGAGTTTGCGCCACTGCACCCAGCCTAGGTGAGAGAGTGAGAGAGA	CTCCATCTCAAAAAAATAAAAATAAAAATAAAAAATGAAAAAAAA	TAGAGTATCTCATAGTTTGTCAGTGATAGAAACAGGTTTCAAACTCAGTCAATCTGACCG 	TTTGATACATCTCAGACACCACTACATTCAGTAGTTTAGATGCCTAGAATAAATA	GGAAGGAGATGGCTCTTCTTGTCTCATTGTGTTTCTTCTGAGTGAG
7501	2 2	7621 7621	7681 7681	7741	7801	7861 7861	7921	7981 7981	8041	8101	8161 8161	8221 8221	8281 8281	8341	8401	8461	8521 8521	8581
Ę	,	7. Op	λ q	λζ Q	λά Q	Oy Dp	o O	oy Dp	oy Db	g ç	ος Og	Oy Dp	Q Dp	oy Db	Oy Db	Oy Dp	Oy Db	ογ, Ob

δλ	8641	AAGGGGAACAGCAGAAAAAAAACAACCGAACTCCTCAGCTGTCATGTTTCCTTTAAAAGTC 870	
qa	8641	CTGTCATGTTTCCTTTAAAAGT	
Qy	8701	TGAAGGAAGGTCCTGGAATGTGACTCCCTTGTTGTTGTTGTTTTTTGGCATTCA 876	
qa	8701	CTGAAGGAAGGTCCTGGAATGTGACTCCCTTGCTCTCTGTTGCTCTTTGGCATTCA 876	
Qy	8761	ICTTIGGACCCTACGCAAGGACTGTAATTGGTCGGGACAGCTAGTGGCCCTGCTGGGC	
qq	8761	TTCTTTGGACCCTACGCAAGGACTGTAATTGGTGGGGACAGCTAGTGGCCCTGGTGGGC	_
oy g	8821	TTCACACACGGTGTCCTCCCTAGGCCAGTGCCTCTGGAGTCAGAACTCTGGTGGTTTTC 8880	_
3 8	9 00	TO A A TO A A TO A TO A TO A TO A TO A	
S 8	88	CCTCAATGAAGTGGAGTAAGCTCTCTCATTTGAGATGGTATAATGGAAGCACCAAGTG 8940	_
Oy	8941	PAGAGGATCCCCAGGTCCTTCCATGGAGCCCACTGGGGTTCCGGTGCACATTAAAAAA 90	_
QQ	8941	96	_
οy	9001	TTCAGGAATTGCTAGATTCTGGGAAATCAGTTCACCATGTTCA 9C	_
QΩ	9001	rcraaccaggacarrcaggaarrgcragarrcrgggaaarcagrrcaccargrrca 90	_
QY	9061	PITITITITICAGACICTATIGCCCAGGCTGGAGTGCAATGGCATGAI 91	_
qq	9061	AGTCTTTTTTTTTTTTTGAGACTCTATTGCCCAGGCTGCAGTGCAATGGCATGAT 91	_
δy	9121	TCTGCCTCCCAGGITCAAGCGATTCTCCTGTCTCAGCCTCCCA 91	_
g	9121	cecrcacreraactreccreccaegricaaecearrerecrereres 91	_
Qγ	9181	GCACCACCATGCCCGGCTAATTTTTGTATTTTTAGTAGA 92	_
QQ	9181	3TAGCTGGGATTACAGGCGTGCACCACCATGCCCGGCTAATTTTTGTATTTTTAGTAGA 92	_
Qy	9241	GGCCAGGCTGGTCTCGAACTCTCCTGACCTCGTGATCCGCC 93	_
qq	9241	AGGITTCACCATGITGGCCAGGCTGGTCTCGAACTCTCCTGACCTCGTGATCCGCC 93	_
Qγ	9301	GCTGAGATTACAGGTGTGAGCCACCCTGCCCAGCCGTCAAA 93	_
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Qγ	9361	TTACTTTATGTTACTACATGCACTTG 942	0
qq	9361	CTTAATATATATATCCAGATGGCATGTTTACTTTATGTTACTACATGCACTTG 94	0
Qy	9421	GCTGCATAAATGTGGTACAAGCATTCTGTGTAAGGGCAGGTGCTTCAGGATACCATAT 9480	0
• qo	9421	CIGCATAAATGIGGTACAAGCATTCIGTCTTGAAGGGCAGGTGCTTCAGGATACCAT	0
Qy	9481	ACAGCTCAGAAGTITCTICTITAGCATIAAAITITAGCAAAGAIATCICATCITCIT 9:	0
qq	9481	TCAGAAGTTCTTCTTTAGGCATTAAATTTTAGCAAAGATATCTCATCTTCT	0
Qy	9541	TTAAACCATTTTCTTTTTTTTTTTTT 9600	0
QD	9541	IAAACCATTTTTTTTTTTTGTGGTTAGAAAGTTATGTAGAAAAAAA	0
ΟŸ	9601	ACCTCATTGTAGAAAAGCTATAAAATGAATACAATTAAAGGTGTTATTAATTA	0
qa	9601	ACGCTCATTGTAGAAAAGCTATAAAATGAATACAATTAAAGCTGTTATTAATTA	0
QY	9661	TGAAAAACTATTAACAACTTGTCTATTACCTGTTAGTATTATTGTTGCATTAAAAATGCA 972	0
qq	9661	TGAAAAACTATTAACAACTTGTCTATTACCTGTTAGTATTATTGTTGCATTAAAATGC	0

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10801 TAAAATCCCCAAATTTTTCATAAAC 10825
   GENERAL INFORMATION:
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                                                              RESULT 12
US-09-503-444A-7
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                                                            9841 CTTTACATTTTGTCTTACGGAATATTTTCATTCAACTGTGGTAGCCGAATTAATCGTGTT
                                                                                                                                                                                 9901 TCTTCACTCTAGGGACATTGTCGTCTAAGTTGTAAGACATTGGTTATTTTACCAGCAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                             10141 CCAGTCTTCACAGTAACACATTTCACTAACACATTTACTAAACATCAGCAACTGTGGCCT
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/note= "Hereditary Hemochromatosis (HH)
gene containing a combination of both
24d1 and 24d2 alleles"
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LOCATION: join(361..436, 3762..4025, 4235..4510, 5606..58
LOCATION: 6040..6153, 7107..7147)
OTHER INFORMATION: /product= "Hereditary Hemochromatosis OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 140.,7319
OTHER INFORMATION: /note= "start and stop positions
OTHER INFORMATION: CDNA containing a combination of
                                                                                                                                                                                                                                                                                Hereditary Hemochromatosis Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8907-0088-999
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                                                                                                                                                                                                                                                                                                                                                                                                       CITY: New York
STATE: New York
COUNTRY: New York
COUNTRY: USA
ZIP: 10036
COMPUTER REAABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect Version 8
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/503,444A
FILING DATE: 14-Feb-2000
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/652,265
FILING DATE: 23-May-1996
FILING DATE: 16-APPL-1996
                                                                                                                                                                                                                                                                                                                                                          1: Pennie & Edmonds LLP
1155 Avenue of the Americas
Sequence 7, Application US/09503444A Patent No. 6228594
                                                                          APPLICANT: Thomas, Winston J.
APPLICANT: Drayna, Dennis T.
APPLICANT: Grana, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchlhashi, Zenta
APPLICANT: Wolff, Roger K.
APPLICANT: Wolff, Roger K.
APPLICANT: Wolff, Hereditary
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 66141
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 10825 Dase pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Poissant, Brian M. REGISTRATION NUMBER: 28,462 REFERENCE/DOCKET NUMBER: 89 TELECOMUNICATION INFORMATION: TELEPHONE: 212-790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       212-869-9741
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1441 TGTAGCACAGTGTTCTGTGGGTCACACGCCGGCCTCAGCACAGTGTTTGGTA 1500
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                                                                                  TAAATAAATCTCGTAGTTCCTCACTTGAGCTGAGCTAAAGCCTGGGGGCTCCTTGAACCTGG
                                                                                                                          AACTCGGGTTTATTTCCAATGTCAGCTGTGCAGTTTTTTCCCCAGTCATCTCCCAAACAGG
                                                                                                                                                                 AAGTTCTTCCCTGAGTGCTTGCCGAGAAGGCTGAGCAAACCCACAGGAGCAGGATCCGCACGG
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                                                                                                                                                                                                                                                                                                    Length 10825
                                                                                                                                                                            Hemochromatosis
                                                                                                                                                                                                                                      /phenotype- "Hereditary Hemochromatosis
                                                   /note= "start and stop positions for genomic sequence surrounding variant for 24d2(G) allele (SEQ ID NO:42)"
                                                                                                              /note= "start and stop positions for genomic sequence surrounding variant for 24d1(A) allele (SEQ ID NO:21)"
                                                                                                                                                                                                                                                                                                                     2;
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Pred. No. 0;
0; Mismatches
 1 24d2 alleles
NO:12)"
                                                                                                                                                               LOCATION: replace(3872, "g")
OTHER INFORMATION: /phenotype=
OTHER INFORMATION: /label= 24d2
                                                                                                                                                                                                                                                          /label= 24d1
                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                       FEATURE:
NAME/KEY: allele
LOCATION: replace(5834, "a")
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OTHER INFORMATION: /label= 24
  and
ID N
                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0%;
Matches 10823; Conservative
  24d1
(SEQ
                    FEATURE:
NAME/KEY:
LOCATION: 3852..3891
OTHER INFORMATION: GONGRER INFORMATION: GENOTHER INFORMATION: for FEATURE:
                                                                                                       .6023
                                                                                           NAME/KEY: -
LOCATION: 5507..602:
OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION:
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Qy Dp	1741	CAAGGGAGAGAGCAGGGAAACAAGTCTTTACCCTTTGATATTTTGCATTCTAGTGGGAGA 1800 	
Qy Db	1801	GATGACAATAAGCAAATGAGCAGAAAGATATACAACATCAGGAAATCATGGGTGTTGTGA 1860 	
Oy Db	1861 1861	GAAGCAGAGAAGTCAGGGCAAGTCACTCTGGGGCTGACACTTGAGCAGAGACATGAAGGA 1920 	
Qy	1921	AATAAGAATGATATTGACTGGGAGCAGTATTTCCCCAGGCAAACTGAGTGGGCCTGGCAAG 1980 	
Oy Dp	1981	TIGGATTAAAAAGGGGTTTTCTCAGCACTACTCATGTGTGTG	
Qy Db	2041	CGGCGTGGGGGTGGGAAGGGGACTACCATCTGCATGTAGGATGTCTAGCAGTATCCTGT 2100	
Qy	2101	CCTCCCTACTCACTAGGTGCTAGGAGCACTCCCCCAGTCTTGACAAACCAAAAATGTCTCT 2160	
O.Y D.D	2161	AAACTITGCCACATGTCACCTAGTAGACAAACTCCTGGTTAAGAAGCTCGGGTTGAAAA 2220 	
O.y D.b	2221	AATAAACAAGTAGTGCTGGGGAGTAGAGGCCAAGAAGTAGGTAATGGGCTCAGAAGAGGA 2280 	
Qy Db	2281 2281	GCCACAAACAAGGTTGTGCAGGCGCCTGTAGGCTGTGGTGTAAATTCTAGCCAAGGAGTA 2340 	
Qy	2341	ACAGTGATCTGTCACAGGCTTTTAAAAGATTGCTCTGGCTGCTATGTGGAAAGCAGAATG 2400 	
Qy Db	2401	AAGGGAGCAACAGTAAAAGCAGGGAGCCCAGCCAGGCAAGCTGTTACACAGTCCAGGCAAG 2460	
QY Db	2461	AGGTAGTGGAGTGGGCTGGGTAGCAGAAAAGGGAGTGACAAACCATTGTCTCCTGAA 2520	
Qy Db	2521	TATATICTGAAGGAAGTTGCTGAAGGATTCTATGTTGTGTGAGAGAAAGAGAAAGAGTTGG 2580	
oy Ob	2581	CTGGGTGTAGTAGCTCATGCCAAGGAGGCCAAGGAGGAGCAGATTCCTGAGCTCAGGA 2640	
Oy Op	2641	GTTCAAGACCAGCCTGGGCAACACCGCAACCCCTTCTCTACAAAAATACAAAAATTA 2700	
Oy Dp	2701	GCTGGGTGTGGTGGCATGCACCTGTGATCCTAGCTACTCGGGAGGCTGAGGTGGAGGGTA 2760	
δλ	2761	. TTGCTTGAGCCCAGGAAGTTGAGGCTGCAGTGACCATGACTGTGCCACTGTACTTCAGC 2820	

3540 3600 3660 3660 3720 3780 3060 3060 3120 3180 3240 3240 3300 3360 3360 3420 3420 3480 3480 3540 3600 3720 3780 TTGCTTGAGCCCAGGAAGTTGAGGCTGCAGTGAGCCATGACTGTGCCACTGTACTTCAGC 2820 CTCCTACTACACATGGTTAAGGCCTGTTGCTCTGTCTCCAGGTTCACACTCTCTGCACTA CCICITCAIGGGIGCCICAGAGCAGGACCIIGGICIIICCCIIGIIIGAAGCIIIIGGGCIA CGTGGATGACCAGCTGTTCGTGTTCTATGATNATGAGAGTCGCCGTGTGGAGCCCCCGAAC CCAGACACACCTGATGGTATGAGTTGATGCAGGTGTGTGGAGCCTCAACATCCTGCTCCC CTCCTACTACACATGGTTAAGGCCTGTTGCTCTGTCTCCAGGTTCACACTCTCTGCACTA TTCTGAGATGGTGAAGGCAGAGGAAAGAGCAGTTTGGGGTAAATCAAGGATCTGCATTTG GGACATGTTAAGTTTGAGATTCCAGTCAGGCTTCCAAGTGGTGAGGCCACATAGGCAGTT GGACATGTTAAGTTTGAGATTCCAGGCTTCCAAGTGGTGAGGCCACATAGGCAGTT CAGTGTAAGAATTCAGGACCAAGGCTGGGCACGGTGGCTCACTTCTGTAATCCCAGCACT CAGTGTAAGAATTCAGGACCAAGGCTGGGCACGGTGGCTCACTTCTGTAATCCCAGCACT TTGGTGGCTGAGGCAGGTAGATCATTTGAGGTCAGGAGTTTGAGACAAGCTTGGCCAACA ATAGTCCCAGGTTTTCAGGAGGCTTAGGTAGGAGAATCCCTTGAACCCAGGAGGTGCAGG ATAGTCCCAGGTTTTCAGGAGGCTTAGGTAGGAGAATCCCTTGAACCCAGGAGGTGCAGG CTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAACTGAAGGAATTATTCCTCAGGATTTGGG TCTAATTTGCCCTGAGCACCAACTCCTGAGTTCAACTACCATGGCTAGACACACCTTAAC CTGGGGGCAGTGAGGGGGTGGCAGCTGTGTGCAGAGAAAAGCACACAAAAGGAAAAGC ACCCAGGACTGTCATATGGAAGAAAGACAGGACTGCAACTCACCCTTCACAAAATGAGGA TGACTTTGTTCTTTATTTTAATTTTATTGGCCTGAGCAGTGGGGGTAATTGGCAATGCCAT TTGCAGTGAGCTGAGATTGTGCCACTGCACTCCAGCCTGGGTGATAGAGTGAGACTCTGT 3841 2761 2881 2941 3001 3001 3061 3121 3181 3241 3241 3301 3361 3361 3421 3421 3481 3481 3541 3541 3601 3661 3721 3721 3781 3781 2821 2821 2881 2941 3061 3121 3181 3301 3601 3661 g QQ QQ qq g Dp δ QQ Qγ Ω qq qq qq qq δy Ω Qγ ŏ ŏ g QC δy QQ δy Op ٥y òγ ΩD δŽ òγ Ω QΥ δλ g Ω δý

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CCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGCAGCTGAGTCAGAGT [1]	TGCATCTTGAAGGAACCAGCAAGTCTGAGGTCTTGTGGGACCAGGGAAGAGGGAATGTGCATGTGTGGAAGGGAAGAGGGAATGTGGTGAAGTCTGAGGAATTGTTTGT		CTGGAGAGGGACTGCCCTCCACCTGCAGCAGTTGCTGGAGCTGGGGGAGAGTGTTTG [AAATTCAGAAATGTCAAGGCCGGGCACGGTGGCTCACCCCTGTAATCCCAGCACTTTGGG AAATTCAGAAATGTCAAGGCCGGGCACGGTGGCTCACCCCTGTAATCCCAGCACTTTGGG AAATTCAGAAATGTCAAGGCCGGGCACGGTGGCTCACCCTGTAATCCCAGCACTTTGGG AGCCGAGGCGGGTGGTCACAAGGTCAGGAGTTTGAGACCAGCCTGACCAACATGGTGAA
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8040 8040 8100 8100 8160 7920 7680 7740 7740 7800 7800 7860 7920 7320 7380 7500 7500 7560 7620 7620 7680 TTACCAGATTTTACACATGTATCTATGCATTTTCTGGACCGTTCAACTTTTCCT TGTCCCAGAAAAAGCATCATGGCTATCTGTGGGTAGTATGATGGGTTTTTAGC IGATAAGGATGATAAAAGCACTTACTTCGTGTCCGACTCTTCTGAGCACCTACTTA JATTACTGCATGCACTTCTTACAATAATTCTATGAGATAGGTACTATTATCCCCAT CITTGGGAGGCCAAAGCGGGTGGATCACGAGGTCAGGAGATCGAGACCATCCTGGC CATGAACCTCAAGCTGCATCTAGAGGCTTCCTTCATTTCCTCCGTCACCTCAGAG rgattgtgatgtgagttgcacagctatgaaggctgtacactgcacgaatggaagag SACCTGAAGAATCACAATAATTTTCTACCTGGTCTCTCCTTGTTCTGATAATGAAA PTTTTAAATGAAGAAAGTGAAGTAGGCCGGGCACGGTGGCTCACGCCTGTAATCCC JTTTCTGAGTTCCTGCATGCCGGTGATCCCTAGCTGTGACCTCTCCCCTGGAACTG CACCTATGTCATTTCATTTCCTATTTTGGAAGAGGACTCCTTAAATTTGGGGGA ATCCTCTCTCTGTGTTACCCAGTAACTCATCTGTCACCAAGCCTTGGGGGATTCTTC ACGAACTCCTTGATTTTAGCCTTCTCTGTTCATTTCCTCAAAAAGATTTCCCCAT

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CTATTTGAATTGCTGGAATCACAGGCCATTGCTGAGCTGCCTGAACTGGGAACACAACAG
                                                                                                                                    AAGGAAAACCAACTCTGATAATCATTGAGTCAAGTACAGCAGGTGATTGAGGACTGC
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Frommal, Gregory S.
APPLICANT: Kronmal, Gregory S.
APPLICANT: Lauer, Peter M.
APPLICANT: Lauer, Peter M.
APPLICANT: Lauer, Peter M.
APPLICANT: Thomas, Winston
APPLICANT: Thomas, Winston
APPLICANT: Touchihashi, Zenta
APPLICANT: Wolff, Megabase Transcript Map: No. 587223
TITLE OF INVENTION: Megabase Transcript Map: No. 587223
CORRESPONDENCE ADDRESS: 31
CORRESPONDENCE ADDRESS: ADDRESSE: TOWNSEND and TOWNSEND and CREW LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: TOWNSEND and TOWNSEND and CKEW STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
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FILING DATE: 01-0CT-1996
CLASSIPICATION: 536
ATTOCNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERNCE/DOCKET NUMBER: 017957-0001C
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                     Sequence 20, Application US/08724394A Patent No. 5872237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acid
EDNESS: not relevant
3Y: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 246240 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNA
                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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94111-3834
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Db 192604 TITCCCGCCCCCAAAGAAGGGGAGAITAACGGGGACGIGCGGCCAGAGCTGGGGAA 192663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Db 192784 GAAAAATCGAAACTAGCTTTTTTTTTTTGGGAGTTTGCAACTTTGGAGGACCTGC 192843
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCAGGATTTAAAAACCAAGGGGGACACTGGATCACCTAGTGTTTCACAAGCAGGTACCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db 192664 ArggGCCCGCGAGCCAGCCGGCGCTTTTCCTGATGCTTTTGCAGACCGCGGTCCTG
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                                                                                                                                                                        Length 246240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTGCTGTAGGAGAAGAAGTAGAAGTTCTGAAAGACCTGTTGCTTTTCACCAGGAAGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              421 CAGGGGCGCTTGCTGCGTGAGTCCGAGGGCTGCGGGGGAACTAGGGGCGCGCGGGGGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                481 GAAAAATCGAAACTAGCTTTTTCTTTGCGCTTGGGAGTTTGCTAACTTTGGAGGACCTGC
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                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                         5
                                                                                                                                                                                               Pred. No. 0;
0; Mismatches
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..246240
; OTHER INFORMATION: /note= "HLA-H.CONTIG"
US-08-724-394A-20
                                                                                                                                                                     Score 10823;
                                                                                                                                                                     100.0%;
100.0%;
                                                                                                                                                                Query Match
Best Local Similarity 100.0
Matches 10823; Conservative
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93	1020 193323	1080 193383	1140 193443	1200 193503	1260 193563	1320 193623	1380 193683	1440 193743	1500 193803	1560 193863	1620 193923	1680 193983	1740 194043	1800 194103	1860 194163	1920 194223	1980 194283	2040 194343
SGCGTTGGGGA	STCTCTAGGGT	CAATTGITCITT CAATTGITCITT CAATTGITCITT		ACAAAGTACTGA ACAAAGTACTGA	GATCTTATTIGA 	TAGAAGTTAACT	rcregitticie rcregitticie	TTTGCCCTGTAG	TGAGTTTTGGTA TGAGTTTTGGTA	ccrecrrccres	CCACTTCATAGC	CATGTTGAGCAG 	CACTGTTCAAGCCC	TCTAGTGGGAGA 	TGGGTGTTGTGA 	AGACATGAAGGA 	GGGCCTGGCAAG	00000000000000000000000000000000000000
CGCGAAAGA	GACCTGGGGTGGAGG 	CCCCACTCTTGGC/ 	TTGAACTGAACAAT TTGAACTGAACAAT	AAGAGGCCTCTCTV AAGAGGCCTCTCTV	TACATICATATCI TACATICATATCI	ACGTTTATTTAC 	KCAAAGAACATAAATAATC 	AGTTGACAGTGAT' AGTTGACAGTGAT'	CAGCACAGCACTTT 	GAGGCATGGCACGG 	CAGAGCTCATGTCT 	AATAATAAATTT AATAATAAAATTT	AGCCATGTGTTGCA 	TIGATATTTIGCAT TIGATATTTIGCAT	CATCAGGAAATCAT 	GACACTTGAGCAG 	CAGGCAAACTGAGT 	TCTGTGTGTGTGT TGTGTGTGTGTGT
resecestes	CCACTTTTGGTGAC	ACCTCGGGCCTTTC 	AGTTTGAACGT AGTTTTGAACGT	GTGCTGTGTAATTA 	CTAAGT	GGAGCTAATAAT 	TTCAGGTTA TTCAGGTTA	CTTCTAATCTT 	ACACGCCGCCT ACACGCCGGCCT	ACACATGACAAGAATG 	CTTTGGTGG 	GCATTAGAGGTTG. 	GTAAATGAGTCCCA GTAAATGAGTCCCA	AAGTCTTTACCCTT	KGAAAGATATACAAC 	rcactctggggctv rcactctggggctv	AGCAGTATTTCC AGCAGTATTTCC	TCAGCACTACTCAT(TCAGCACTACTCAT(
CAGAACGAATGC	TCACCATTCCACO	SAGAGGCCT 	GAAAATTAAGTATATGTT) 	TTATTGATTTGCAATG	GTAAGCAATGCACTCACTT 	SCATAGGGAGGTA 	FTATATAACTCTT 	TCAAGTACTACAGCTG TCAAGTACTACAGCTG	TGTTCTGTGGGTC. TGTTCTGTGGGTC.	CACATTT 	CAATGGTACACTGGC 	TTAAACATCACACTG	rgtttacaagi rgtttacaagi	GAGCAGGGAAACA/ 	AAGCAAATGAGCAC 	AAGTCAGGGCAAGT(ATATTGACTGGG 	AAGCGGGTTTTCT AAGCGGGTTTTCT
TTTCCACC	TCTGAATTCTT TCTGAATTCTT	GGGAGGCTCCT(GCCTGGAAAAT 	CTAGGCTTTA1 	TAATGAACATG	TTTTCACTAGGG	GGAATTCAGATTATA 	ATGTTATTTCI	TGTAGCACAG TGTAGCACAG	CTACGTGTAT(CTACGTGTAT(CAAATTTATT 	TATGATTC	AAATATTCAT	CAAGGGAGA 	GATGACAAT GATGACAAT	GAAGCAGAG GAAGCAGAG	AATAAGAATG	1 TTGGATTAAAAGC
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194643 194944 GITCAAGACCAGCCIGGGCAACACAGCAAAACCCCITCTCTACAAAAAATACAAAATTA 195003 195063 195123 195303 195363 195423 CGGCGTGGGGGTGGGAAGGGGGACTACCATCTGCATGTAGGATGTCTAGCAGTATCCTGT 2100 QY 2341 ACAGTGATCTGTCACAGGCTTTTAAAAGATTGCTCTGGCTGCTATGTGGAAAGGAGAATG 2400
Db 194644 ACAGTGATCTGTCACAGGCTTTTAAAAGATTGCTCTGGCTGCTGCTGGAAAGGAAAGG 194703 194823 194883 194583 2940 3060 2640 2700 2760 3000 2460 2340 195364 CAGTGTAAGAATTCAGGACCAAGGCTGGCACGGTGGCTCACTCTGTAATCCCAGCAC 195244 TTCTGAGATGGTGAAGGGAAGGGCAGTTTGGGGTAAATCAAGGATCTGCATTTG 2941 ITCTGAGATGGTGAAGGCAGAGGAAAGAGCAGTTTGGGGGTAAATCAAGGATCTGCATTTG 195304 GGACATGTTAAGTTTGAGATTCCAGTCAGCTTCCAAGTGGTGAGGCCACATAGGCAGTT AAGGGAGCAACAGTAAAAGCAGGGAGCCCAGGCAGGAAGCTGTTACACAGTCCAGGCAAG GTTCAAGACCAGCCTGGGCAACACAGCAAAACCCCTTCTCTACAAAAATACAAAATTA GCTGGGTGTGGTGGCATGCACCTGTGATCCTAGCTACTCGGGAGGCTGAGGTGGAGGTA 195004 CCTGGGTGTGGTGCATCCTGTGATCCTAGCTACTCGGGAGGCTGAGGTGCAGGTA TTGCTTTGAGCCCAGGAAGTTGAGGCTGCAGTGAGCCATGACTGTGCCACTGTACTTCAGC TGACTITIGITCITIATITIAATITIATITGGCCTGAGCAGTGGGGGTAATITGGCAATGCCAT GGACATGTTAAGTTTGAGATTCCAGTCAGGCTTCCAAGTGGTGAGGCCACATAGGCAGTT CAGTGTAAGAATTCAGGACCAAGGCTGGCACGGTGGCTCACTTCTGTAATCCCAGCACT AAACTTTGCCACATGTCACCTAGTAGACAAACTCCTGGTTAAGAAGCTCGGGTTGAAAAA AGGTAGTGGAGTGGGTGGGAACAGAAAAGGGAGTGACAAACCATTGTCTCCTGAA TATATICIGAAGGAAGTIGCTGAAGGATICTATGTIGTGTGAGAGAAAGAAATIGG CTGGGTGTAGTAGCTCATGCCAAGGAGGAGGCCAAGGAGGAGCAGATTCCTGAGCACAGGA AATAAACAAGTAGTGCTGGGGAGTAGAGGCCAAGAAGTAGGTAATGGGCTCAGAAGAGGA GCCACAAACAAGGTTGTGCAGGCGCCTGTAGGCTGTGGTGTAATTCTAGCCAAGGAGTA CCTCCCTACTCACTAGGTGCTAGGAGCACTCCCCCAGTCTTGACAACAAAAATGTCTCT 2761 3001 3061 194824 2581 2641 2701 195064 2881 2161 2221 2281 2401 Db 194704 2461 2521 2041 2101 Db 194404 194464 Db 194524 194584 194344 οp qq QQ g QQ οp Dβ g g q δy δλ ğ οy Qy ŏ Οy g ò ŏ q QΥ οy g δ ò δλ δ δý

⊣	12	TTGGTGGCTGAGGCAGGTAGATCATTTGAGGTCAGGAGTTTGAGACAAGCTTGGCCAACA 3180 }
OY	3181	TGGTGAAACCCCATGTCTACTAAAAATACAAAATTAGCCTGGTGTGGTGGCGCACGCCT 3240
Db 19	95484	
Qy Db 19	3241 95544	ATAGTCCCAGGTTTTCAGGAGGCTTAGGTAGGAGAATCCCTTGAACCCAGGAGGTCCAGG 3300
QY Db 19	3301 95604	TTGCAGTGAGCTGAGATTGTGCCACTGCACCTGGGTGATAGAGTGAGACTCTGT 3360
0y	3361	CTCAAAAAAAAAAAAAAAAAAAAAAAAAAACTGAAGGAATTATCCTCAGGATTTGGG 3420
Db 19	95664	
OY Db 19	3421 95724	TCTAATTIGCCCTGAGCACCAACTCCTGAGTTCAACTACCATGGCTAGACACCTTAAC 3480
Qy	3481	ATTICTAGAATCCACCAGCTTTAGTGGAGTCTGTCTAATCATGAGTATTGGAATAGGAT 3540
Db 19	95784	
0y	3541	CTGGGGGCAGTGAGGGGGTGGCAGCCACGTGTGGCAGAAAAGCACACAAGGAAAGAGC 3600
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Qy Db 19	3601 95904	ACCCAGGACTGTCATATGGAAGAAGACAGGACTGCAACTCACCTTCACAAATGAGGA 3660
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Db 19	96024	
Qy Db 19	3781 96084	CCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCTTGTTTGAAGCTTTGGGCTA 3840
Oy	3841	CGTGGATGACCAGCTGTTCGTGTTCTATGATNATGAGAGTCGCCGTGTGGAGCCCCGAAC 3900
Db 19	96144	
0y	3901	TCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGGAGCTGAGTCAGAGTCTGAA 3960
Db 19	96204	
0y	3961	AGGGTGGGATCACATGTTCACTGTTGGACTATTATGGAAAATCACAACCACAG 4020
Db 19	96264	
0y	4021	CAAGGGTATGTGGAGAGGGGCCTCACCTTCCTGAGGTTGTCAGAGCTTTTCATCTTTTC 4080
0b 19	96324	
0y	4081	ATGCATCTTGAAGGAAACAGCTGGAAGTCTGAGGTCTTGTGGGAGGAAGAGGAAGAGAAG 4140
Db 19	96384	
Oy Db 15	4141	GAATTTGCTTCCTGAGATCATTTGGTCCTTGGGGATGGTGGAAATAGGGACCTATTCCTT 4200
δλ	4201	TGGTTGCAGTTAACAAGGCTGGGGATTTTTCCAGAGTCCCACACCCTGCAGGTCATCCTG 4260

Db 196984 TGAGACAGCCACAAGTCATGGGTTTAATTTCTTTTCTCCATGCATATGGCTCAAAGGGAA 197043 Db 197164 AGGCCGAGGCGGTGGTCACAAGGTCAGGAGTTTGAGACCAGCCTGACCAACATGGTGAA 197223 197343 197523 196623 196803 196804 GACCAACAAGGTATGGTGGAAACACACTTCTGCCCCTATACTCTAGTGGCAGAGTGGAG 196863 196923 197163 197283 197403 197463 5160 4440 4620 4680 4740 4800 4980 5100 5340 DD 197284 GCTAATTGGAAGGCTGAGGAGGAGGAGCATGAGCTTGGGAAGCGGGAAGCTGCAACGTGGAAGCTGGAAGTTGCAAGGTTGCAAGGAGCAGGAGCATGAACCTTGGAAGCGGGAAGCTGCAACA CTCCTAGGTTGACCCAGGTGAAACTGACCATCTGTATTCAATCATTTTCAATGCACATAA GCCTGTGAAATGCAAGAAGACAACAGTACCGAGGGCTACTGGAAGTACGGGTATGATGG Db 196684 TGGCCCACCAAGCTGGAGTGGGAAAGCCACAAGATTCGGGCCAGGAGAACAGGACCTAC 4801 AAATTCAGAAATGTCAAGGCCGGCACGGTGGCTCACCCCTGTAATCCCAGCACTTGGG AAATTCAGAAATGTCAAGGCCGGGCACGGTGGCTCACCCCTGTAATCCCAGCACTTTGGG 4921 ACCCGTCTCTAAAAAAAAATACAAAATTAGCTGGTCACAGTCATGCGCACCTGTAGTCCCA ACCCGTCTCTAAAAAAAAAACAAAAAATTAGCTGGTCACAGTCATGCGCCACCTGTAGTCCCA GCCAAGATCGCGCCACTGCACTCCAGCCTAGGCAGCAGAGTGAGACTCCATCTTAAAAAA 5101 AAAAAAAAAAAAAAAAAAAAAGAGATTCAGAGATCTCAGGCTATCATATGAATACCAGGACAAA CTGGAGAGGGACTGCCCTGCACAGCTGCAGCTTGCTGGAGCTGGGGGAGAGGTGTTTTG TCCAAATTCTGGGAAGGGACTTTCTCAATCCTAGAGTCTCTACCTTATAATTGAGATGTA GTGTCTATGGCCCTTGCTTTTATTTAACCAATAATCTTTTGTATATTTATACCTGTTAA AGGCCGAGGCGGGTGGTCACAAGGTCAGGAGTTTGAGACCAGCCTGACCAACATGGTGAA GCTAATTGGAAGGCTGAGGCAGGAGCATCGCTTGAACCTGGGAAGCGGAAGTTGCACTGA AGAACATAGCAATAATCACTGAAGCTACCTATCTTACAAGTCCGCTTCTTATAACAATGC TGGCCCACCAAGCTGGAAAAGGCACAAAATTCGGGCCAGGAAACAGGGCCTAC GACCAACAAGGTATGGTGGAAACACACTTCTGCCCCTATACTCTAGTGGCAGAGTGGAGG TGAGACAGCCACAAGTCATGGGTTTAATTTCTTTTTCTCCATGCATATGGCTCAAAGGGAA 5041 4441 5281 4261 4381 4501 4681 4861 5221 196504 196564 196744 4561 Db 196864 4621 Db 196924 4741 Db 197044 Db 197104 Db 197224 4981 197344 197524 g g a g δŏ qq ΩŽ ð QΥ δλ δŏ δy δy δλ δλ ò ò QΥ δ δ

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197643	5400 197703	5460 197763	5520 197823	5580 197883	5640 197943	5700 198003	5760 198063	5820 198123	5880 198183	5940 198243	6000 198303	6060 198363	6120 198423	6180 198483	6240 198543	6300 198603	6360 198663	6420 198723
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Db 197584	Oy 5341 Db 197644	Qy 5401 Db 197704	Qy 5461 Db 197764	Oy 5521 Db 197824	Oy 5581 Db 197884	Qy 5641 Db 197944	Oy 5701 Db 198004	Qy 5761 Db 198064	<i>Qy</i> 5821 Db 198124	Qy 5881 Db 198184	Oy 5941 Db 198244	Qy 6001 Db 198304	Qy 6061 Db 198364	Oy 6121 Db 198424	Oy 6181 Db 198484	Oy 6241 Db 198544	Qy 6301 Db 198604	Oy 6361 Db 198664
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Db 198724 TCTCAGAACCCAAATCTGGTAGGGAATGAAATTGATAGCAAGTAAATGAAATGAAATGAAAG 198783 198903 TTAGGTGAGGTTGAGGAGGTGTACACAGAGGGAGCAACCATGCCAAGTAGGA 198963 199143 199203 199323 199383 199443 199563 199743 7020 7140 7200 ACCCCATGAGGTCCTAAAGCAGGCAGGAAGCAAATGCTTAGGGTGTCAAAGGAAAGAATG Db 198844 ATCACATTCAGCTGGGGATCAAGATAGCCTTCTGGATCTTGAAGGAGAAGCTGGATTCCA TCTCAGAACCCCAAATCTGGTAGGGAATGAAATTGATAGCAAGTAAATGTAGTTAAAGAAG ACCCCATGAGGTCCTAAAGCAGCAGGAAGCAAATGCTTAGGGTGTCAAAGGAAAGAATG ATCACATTCAGCTGGGGATCAAGATAGCCTTCTGGATCTTGAAGGAGAAGCTGGATTCCA AGCTATCACTCACCAATTATGCATTTCTACCCCCTGAACATCTGTGGTGTAGGGAAAGA GAATCAGAAAGAAGCCAGCTCATACAGAGTCCCAAGGGTCTTTTGGGATATTGGGTTATGA **AATGTGTTGTTAAGAAGTTAGATGAGAGGTGAGAGAGCCAGTTAGAAAGCCAATAAGCAT** TTCCAGATGAGAGATAATGGTTCTTGAAATCCAATAGTGCCCAGGTCTAAATTGAGATGG TGAGTGACACGCAGCCTGCAGACTCACTGTGGGAAGGAGACAAAACTAGAGACTCAAAGA GGGAGTGCATTTATGAGCTCTTCATGTTTCAGGAGAGAGTTGAACCTAAACATAGAAATT TTAGGTTTCTGAGTTCCTGCATGCCGGTGATCCCTAGCTGTGACCTCTCCCCTGGAACTG TCTCTCATGAACCTCAAGCTGCATCTAGAGGCTTCCTTCATTTCCTCCGTCACCTCAGAG TTAGGTGAGGTTGAAGATGATGGGAGGTCTACACAGAGGAGCAACCATGCCAAGTAGGA GAGTATAAGGCATACTGGGAGATTAGAAATAATTACTGTACCTTAACCCTGAGTTTGCGT GTGAATGAGGAAAATAAGGAAGAAGAGAAGAGGCAAGATGGTGCCTAGGTTTGTGATGCCT CTTTCCTGGGTCTCTTGTCTCCACAGGAGGAGCCATGGGGCCACTACGTCTTAGCTGAACG 6961 6421 6481 6541 6601 6661 6721 6781 Db 199084 6901 7021 7081 7141 7261 7381 Db 198784 Db 199264 Db 199384 Db 199444 7321 Db 199684 Db 198904 Db 198964 199024 Db 199324 7201 Db 199504 Db 199564 Db 199624 ò õ ŏ ò ò δ q δ à ò οy οy δ δy δ ŏ ά

Òy Db	7501 199804	CTTACATGATTCATTTTAACATCTGAGAAAGCTTTGAACCCTGGGACGTGGCTAGTCAT 7560
QY Db	7561 199864	AACCTTACCAGATTTTTACACATGTATCTATGCATTTTCTGGACCCGTTCAACTTTTCCT 7620
Qy Db	7621 199924	TTGAATCCTCTCTGTGTTACCCAGTAACTCATCTGTCACCAAGCCTTGGGGATTCTTC 7680
QY	7681 199984	CATCTGATTGTGATGTGAGTTGCACAGCTATGAAGGCTGTACACTGCACGATGGAAGG 7740
QY	7741	GCACCTGTCCCAGAAAAAGCATCATGGCTATCTGTGGGTAGTATGATGGGTGTTTTTAGC 7800
Qy Db	7801 200104	AGGIAGGAGCAAATAICITGAAAGGGGTTGTGAAGAGGTGTTTTTTCTAATTGGCATGA 7860
Qy Db	7861	AGGIGTCAFACAGAFITGCAAAGTTTAATGGTGCCTTCAFTTGGGATGCTACTCTAGTAT 7920
Qy Db	7921	TCCAGACCTGAAGAATCACAATAATTTTCTACCTGGTCTCTTCTTGTTCTGATAATGAAA 7980
oy ob	7981	attatgataaggatgataaaagcacttacttcgtgtccgactcttctgagcacctactta 8040
Qy Dp	8041	CATGCATTACTGCACTTCTTACAATAATTCTATGAGATAGGTACTATTATCCCCAT 8100
Qy Db	8101	TICTTTTTAAATGAAGAGAGAGGAGGGCGGGCACGGTGGCTCACGCCTGTAATCCC 8160
QY Dp	8161	AGCACTTTGGGAGGCCAAAGCGGGTGGATCACGAGGTCAGGAGTCGAGACCATCCTGGC 8220
QY	8221 200524	TAACATGGTGAAACCCCCATCTCTAATAAAAATACAAAAATTAGCTGGGCGTGGTGGGG 8280
Qy Db	8281 200584	ACGCCTGTAGTCCCAGCTACTCGGAAGGCTGAGGCAGGAATGGCATGAACCCAGGAGG 8340
Qy Db	8341	CAGAGCTTGCAGTGAGCCGAGTTTGCGCCACTGCACTAGGTGAGTGA
QV Db	8401	CTCCATCTCAAAAAAATAAAAATAAAAATAAAAAATGAAAAAAAA
Qy Db	8461 200764	TAGAGTATCTCATAGTTTGTCAGTGATAGAAACAGGTTTCAAACTCAGTCAATCTGACCG 8520
Qy	8521 200824	TITGATACATCICAGACACCACTACATICAGIAGITITAGAIGCCIAGAATAAAIAGAGAA 8580
οy	8581	GGAAGGAGATGGCTCTTCTTCTTCTTCTTTTTTTTTTTT

201543 201603 201723 201843 201903 ACGCTCATTGTAGAAAAGCTATAAAATGAATACAATTAAAGCTGTTATTTAATTAGCCAG 201963 201183 201363 201423 201483 201663 201783 200943 201063 201243 201303 201003 201123 9540 8940 9240 9360 9420 9480 9720 9000 9060 9300 TGAAAAACTATTAACAACTTGTCTATTACCTGTTAGTATTATTGTTGCTTAAAAATGCATTAATAGTTGTTGTTGTTAAAAATGCA ACGCTCATTGTAGAAAAGCTATAAAATGAATACAATTAAAGCTGTTATTTAATTAGCCAG 201364 AAAGAGTCTTTTTTTTTTTTTTGAGACTCTATTGCCCAGGCTGGAGTGCAATGGCATGAT 201544 GACAGGGTTTCACCATGTTGGCCAGGCTGGTCTCGAACTCTCCTGACCTCGTGATCTCGCC 201184 CCTCAATGAAGTGGAGTAAGCTCTCTCATTTTGAGATGGTATAATGGAAGCCACCAAGTG GCTTAGAGGATGCCCAGGTCCTTCCATGGAGCCACTGGGGTTCCGGTGCACATTAAAAAA 201424 CTCGGCTCACTGTAAACCTCTGCCTCCCCAGGTTCAAGCGATTCTCCTGTCTCAGCCTCCCCA AGTAGCTGGGATTACAGGCGTGCACCATGCCCGGCTAATTTTTGTATTTTTAGTAGA TGCCTCGGCCTCCCAAAGTGCTGAGATTACAGGTGTGAGCCACCCTGCCCAGCCGTCAAA AGAGTCTTAATATATATCCAGATGGCATGTGTTTTACTTTATGTTACTACATGCACTTG GCTGCATAAATGTGGTACAAGCATTCTGTCTTGAAGGGCAGGTGCTTCAGGATACCATAT CCTGAAGGAAGGTCCTGGAATGTGACTCCCTTGCTCTCTGTTGCTCTTTTGGCATTCA CCTCAATGAAGTGGAGTAAGCTCTCTCATTTTGAGATGGTATAATGGAAGCCACCAAGTG AAAAICTAACCAGGACATICAGGAAIIGCTAGAITCTGGGAAAICAGIICACCAIGIICA AAAGAGTCTTTTTTTTTTTTGAGACTCTATTGCCCAGGCTGGAGTGCAATGGCATGAT CTCGGCTCACTGTAACCTCTGCCTCCCAGGTTCAAGCGATTCTCCTGTCTCAGCCTCCCA GACAGGGTTTCACCATGTTGGCCAGGCTGGTCTCGAACTCTCCTGACCTCGTGATCCGCC GAAGGGGAACAGCAGAAACAACCAACTGATCCTCAGGTGTCATGTTTCCTTTAAAAGTC TITCITIGGACCCTACGCAAGGACTGTAATTGGTGGGGACAGCTAGTGGCCCTGCTGGGC 8941 9061 9241 9301 9361 9421 9541 9601 1996 9001 201304 9181 201484 201604 201664 9481 201784 201844 201904 8641 8761 9121 201724 8701 8881 201244 200884 Db 200944 201004 201064 qq qq qq qq g Dp Qγ qq gg δλ qq g δ рp δy q g QΥ qq qq δ δŏ δy ò ò δ δŏ pp δ g δy QΫ δy ŏ ŏ

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DD 192424 TCAGGATTTAAAAACCAAGGGGACACTGGATCACCTAGTGTTTCACAAGCAGGTACCTT 192483
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Sequences and Antibodies Thereto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
AURICATION NUMBER: US/08/724,394A
FILING DATE: 01-OCT-1996
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San Francisco
                 Db 203104 TAAAATCCCCAAATTTTTCATAAAC 203128
                                                                                                                                  ; Sequence 21, Application US/08724394A; patent No. 5872237; GENERAL INFORMATION:
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ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 0179
TELECOMMUNICATION INFORMATION:
TELECHONE: 415-576-0200
TAAAATCCCCAAATTTTTCATAAAC
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APPLICANT: Tsuchihashi, Zenta
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not relevant
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LoCATION: 1..246240
GTHER INFORMATION: /note-
US-08-724-394A-21
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INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pairs
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Lauer, Peter M.
Ruddy, David A.
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ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ADDRESSEE: TOWNSEND and
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TITLE OF INVENTION: Megaba
TITLE OF INVENTION: Sequer
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Best Local Similarity 100.0
Matches 10823; Conservative
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Kronmal, Grego
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	181 CTGCTGTAGGAGAGAGAGACT 	241 TTACTGGGCATCTCCTGAGCCTAG 	301 TTTCCCGGCCCCCAAAAGAAGGG 	361 ATGGGCCGGGAGCCAGGCCGGGGT 	421 CAGGGCGCTTGCTGCGTGAGTCCGA 	481 GAAAATCGAAACTAGCTTTTCTTT 	541 TCAACCCTATCGCAAGCCCCTCT	601 CTACCACTGAACTGCAGATAGGGT 	661 CCCGGCTCTGCGGAGTGACTTTTG 111111111111111111111111111111111	721 TAAATAAATCTCGTAGTTCC 	781 AACTCGGGTTTATTTCCAATGTCAG 	841 AAGTTCTTCCCTGAGTGCTTC	901 GGTTTCCACCTCAGAACGAATGCGTT 	961 TCTGAATTCTTCACCAT 	1021 GGGAGGCTCCTGAGAGAG 	1081 GCCTGGAAAATTAAGTATATGTTAG 	1141 CTAGGCTTFATTGATTGCAATGTGCTGT0 	1201 TAATGAACATGTAAGCAATGCACT
,	Qy	QY	QY	QY	QY	Qy	QY	0y	OY	QY	QY	QY	0y	0y	QY	Qy	Oy	Oy
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Db 193984 AAATATTCATTGATTACAAGTGTAAAATGAGTCCCAGCCATGTGTTGACGCC 194043 194643 Db 194104 GATGACAATAAGCAAATGAGCAGAAAGATATACAACATCAGGAAATCATGGGTGTTGTGA 194163 194283 194463 Db 194464 AAACTTTGCCACATGTCACCTAGTAGACAACTCCTGGTTAAGAAGCTCGGGTTGAAAA 194523 194103 2100 2160 2280 1920 1980 CAAATTTATTCAATGGTACACTGGGCTTTGGTGGCAGAGCTCATGTCTCCACTTCATAGC 1620 2341 ACAGTGATCTGTCACAGGCTTTTAAAAGATTGCTCTGGCTGCTATGTGGAAAGCAGAATG 2400 1381 ATGTTATTTCAAGTACTACAGCTGCTTCTAATCTTAGTTGACAGTGATTTTGCCCTGTAG 1440 TTTTCACTAGGCATAGGGAGGTAGGAGCTAATAATACGTTTATTTTACTAGAAGTTAACT 1320 CCTCCCTACTCACTCACTGCTAGGGGCACTCCCCCAGTCTTGGGGAAAAATGTCTT GCCACAAACAAGGTTGTGCAGGCGCTGTAGGCTGTGGATTTTTAGTTGTAGCCAAGGAGTA 1741 CAAGGGAGAGAGCAGGGAAACAAGTCTTTACCCTTTGATATTTTGCATTCTAGTGGGAGA GATGACAATAAGCAAATGAGCAGAAAGATATACAACATCAGGAAATCATGGGTGTTGTGA AATAAGAATGATTGACTGGGAGCAGTATTTCCCAGGCAAACTGAGTGGGCCTGGCAAG AAATATTCATTGTTTACAAGTGTAAATGAGTCCCAGCCATGTGTTGCACTGTTCAAGCCC 1861 GAAGCAGAGAAGTCAGGGCAAGTCACTCTGGGGCTGACACTTGAGCAGACATGAAGGA 2041 CGGCGTGGGGGTGGGAAGGGGGGACTACCATCTGCATGTAGGATGTCTAGCAGTATCCTGT CCTCCCTACTCACTAGGTGCTAGGAGCACTCCCCCAGTCTTGACAACCAAAATGTCTCT AATAAACAAGTAGTGCTGGGGAGTAGAGGCCAAGAAGTAGGTAATGGGCTCAGAAGAGGA GCCACAAACAAGGTTGTGCAGGCGCCTGTAGGCTGTGGTGTAATTCTAGCCAAGGAGTA CTACGTGTATCCACATTTTACACATGACAAGAATGAGGCATGGCACGGCCTGCTTCCTGG 2161 2221 1801 2101 2281 1261 1501 1561 1681 Db 194164 1921 Db 194224 1981 Db 194344 Db 194404 Db 194524 1321 οy QQ g qq οy οy δλ δy δŏ δy δŽ Ω ŏλ δλ δ δλ δŏ δğ

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Qy Dp	2461	aggtagtggagtgggtgggtgggaacagaaaagggagtgacaaaccattgtcttgaa 25 	.20 .4823
Qy Dp	2521	TATATTCTGAAGGAAGTTGCTGAAGGATTCTATGTTGTGAGAGAGA	.80 14883
5 g	2581	CTGGGTGTAGTAGCTCATGCCAAGGAGGAGGCCAAGGAGCAGCAGATCCTGAGCTCAGGA 26 	.40 14943
Oy Dp	2641	GTTCAAGACCAGCCTGGGCAACACAGCAAAACCCTTCTCTACAAAAATACAAAAATTA 27 	000
9 6	2701	GCTGGGTGTGGTGGACTGCTGTGATCCTAGCTACTCGGGAGGTGAGGTGGAGGTA 27	,60 95063
oy Oy	2761	TIGCTIGAGCCCAGGAAGTIGAGGCTGCAGTGAGCCAIGACTGTGCCACTGTACCTTCAGC 28	820 95123
Oy Op	2821	CTAGGTGACAGAGCAAGACCCTGTCTCCCCTGACCCCTGAAAAAGAGAAGAGTTAAAGT 28 	880 95183
oy Db	2881	TGACTITGIICITIATIITAATITIATIGCCIGAGCAGIGGGGTAATIGGCAATGCCAT 29 	940 95243
Q Db	2941	TTCTGAGATGGTGAGGGGGGGGGGGGGGGGTTGGGGTAAATCAAGGATCTGCATTTG 3C 	000 95303
Qy Db	3001	GGACATGTTAAGTTTGAGATTCCAGTCAGGCTTCCAAGTGGTGAGGCCACATAGGCAGTT 3(060 95363
Oy Dp	3061	CAGTGTAAGAATTCAGGACCAAGGCTGGGCACGGTGGCTCACTTCTGTAATCCCAGCACT 31	120 95423
Qy Db	3.	rgctgaggcaggtagarcattgaggtcaggagtttgagacaagcttggccaaca 3 	180 95483
O D	3181	TGGTGAAACCCCATGTCTACTAAAAATACAAAAATTAGCCTGGTGTGGTGGGCGCACGCCT 3:	240 95543
oy D	3 195	TCCCAGGTTTTCAGGAGGCTTAGGTAGGAGAATCCCTTGAACCCAGGAGGTGCAGG 3	300 95603
QQ QD	3301	TTGCAGTGAGCTGAGATTGTGCCACTGCACTCCAGCCTGGGTGATAGAGTGAGACTCTGT 3	360 95663
à à	3361	CTCAAAAAAAAAAAAAAAAAAAAAAAAAACTGAAGGAATTATTCCTCAGGATTTGGG 3 	420 95723
οy	3421	TCTAATTTGCCCTGAGCACCAACTCCTGAGTTCAACTACCATGGCTAGACACCCTTAAC 3	480

724 481	TCTAATTTGCCCTGAGCACCAACTCCTGAGTTCAACTACCATGGCTAGACACCTTAAC ATTTCTAGAATCCACCAGGCTTTAGTGGAGTCTGTCTAATCATGAGTATTGGAATAGGAT	9578
CTG	FTCTAGAATCCACCAGCTTTAGTGGAGTCTGTCTAATCATGAGTATTGGAATAGGA GGGCCAGTGAGGGGGGGGGG	195843 3600 195903
AC AC	GAGGACTGTCATATGGAAGAAAGACAGGA 	95
워드앙	AGACACAGCT AGACACAGCT	3720 196023
5=5	CTCCTACTACACATGGTTAAGGCCTGTTGCTCTGTCTCCAGGTTCACACTCTCTGCACTACTACTACTACTACTACTACTACTACTACTACTACT	3780 196083
ひーひ	CTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCTTGTTTGAAGCTTTGGGCTA 	3840 196143
<u> </u>	GETGGATGACCAGCTGTTCTATGATNATGAGATCGCCGTGTGGAGCCCCGAAC 	3900 196203
	TCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGCAGCTGAGTCAGAGTCTGAA 	3960 196263
~ ~	AGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTATGGAAAATCACAACCACAG 	4020 196323
	CAAGGGTAIGIGGAGAGGGGCCTCACCTTCCTGAGGTTGTCAAGACCTTTCATCTTTTC 	4080 196383
	ATGCATCTTGAAGGAAACAGCTGGAAGTCTGAGGTCTTGTGGGAGCAGGAAGAGGGAAG 	4140 196443
	GAATTIGCTICCIGAGAICATIGGICCTIGGGGAIGGIGGAAAIAGGGACCTATICCTI 	4200 196503
	TGGTTGCAGTTAACAAGGCTGGGGATTTTTCCAGAGTCCCACACCCTGCAGGTCATCTG 	4260 196563
	GGCTGTGAAATGCAAGAACAACAGTACCGAGGGCTACTGGAAGTACGGGTATGATGGG 	4320 196623
	CAGGACCACCTTGAATTCTGCCCTGACACACTGGATTGGAGAGCAGCAGAACCCAGGCCC 	4380 196683
	TGGCCCACCAAGCTGGAGTGGGAAAGGCACAAGATTCGGGCCAGGAGAACAGGGCCTAC 	4440 196743
	CTGGAGAGGGACTGCCCTGCACAGCTGCAGCAGTTGCTGGAGCTGGGGAGAGGTGTTTG 	4500 196803
	GACCAACAAGGTATGGTGGAAACACACTTCTGCCCCTATACTCTAGTGGCAGAGTGGAGG 	4560 196863

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QY	4561	AGGTTGCAGGCACGGAATCCCTGGTTGGAGTTTCAGAGGTGGCTGAGGCTGTGTGCCTC	4620
Db	196864		196923
Oy	4621	TCCAAATTCTGGGAAGGGACTTTCTCAATCCTAGAGTCTCTACCTTATAATTGAGATGTA	4680
Dp	196924		196983
Qy	4681	TGAGACAGCCACAAGTCATGGGTTTAATTTCTTTTCTCCATGCATATGGCTCAAAGGGAA	4740
Db	196984		197043
Qy	4741	GTGTCTATGGCCCTTGCTTTTATTTAACCAATAATCTTTTGTATATTTATACCTGTTAA	4800
Db			197103
Qy	4801 197104	AAATTCAGAAATGTCAAGGCCGGGCACGTGGCTCACCCCTGTAATCCCAGCACTTTGGG	4860 197163
Qy	4861	AGGCCGAGGCGGGTGGTCACAAGGTCAGGAGTFTGAGACCAGCCTGACCAACATGGTGAA	4920
Db	197164		197223
QY	4921	ACCCGTCTCTAAAAAATACAAAAATTACCTGGTCACAGTCATGGGCACCTGTAGTCCCA	4980
Db	197224		197283
Qy	4981	GCTAATTGGAAGGCTGAGGCAGGATCGCTTGAACCTGGGAAGCGGAAGTTGCACTGA	5040
Db	197284		197343
Qy	5041	GCCAAGATCGCGCCACTGCACTCCAGCCTAGGCAGAGAGAG	5100
Db	197344		197 4 03
Qy	5101	AAAAAAAAAAAAAAAAAAAAAAATTCAAAATTCTCAACTATCATC	5160
Db	197404		197463
Qy	5161	AIATCAAGTGAGGCCACTTATCAGAGTAGAACAATCCTTTAGGTTAAAAGTTTCTTTC	5220
Db	197464		197523
Qy	5221	AGAACATAGCAATAATCACTGAAGCTACCTATCTTACAAGTCCGCTTCTTATAACAATGC	5280
Db	197524		197583
Oy	5281	CTCCTAGGTTGACCCAGGTGAACTGACCATCTGTATTCAATCATTTTCAATGCACATAA	5340
Dp	197584		197643
Qy	5341	AGGGCAATTTTATCTATCAGAACAAAGAACATGGGTAACAGATATGTATTACATGTG	5400
Db	197644		197703
Oy	5401	AGGAGAACAAGCTGATCTGACTGCTCTCCAAGTGACACTGTGTTAGAGTCCAATCTTAGG	5460
Op			197763
Qy	5461	ACACAAAATGGTGTCTCTCTGTAGCTTGTTTTTTTCTGAAAAGGGTATTTCCTTCC	5520
Dp	197764		197823
Qy	5521	AACCTATAGAAGGAAGTGAAAGTTCCAGTCTTCCTGGGAAGGGTAAACAGATCCCCTGTC	5580
Db	197824		197883
Oy	5581	CTCATCCTTCCTTTCCTGTCAAGTGCCTCCTTTGGTGAAGGTGACACATCATGTGACC	5640
Dp	197884		197943

198123 198183 198243 198543 198843 198303 198423 198483 198663 198723 199023 198903 5700 5760 5940 0009 0909 6120 6180 6240 6300 6360 6420 6540 0999 6720 6721 AGCTATCACTCACCAATTATGCATTTCTACCCCCTGAACATCTGTGGTGTAGGGAAAAGA 6780 Db 198064 CCCAATGGGGATGGGACTACCAGGCTGGATAACCTTGGCTGTACCCCTGGGGAAGAG 198124 CAGAGATATACGTGCCAGGTGGAGCACCCAGGATCAGCCCTCATTGTGATCTGG 198184 GGTATGTGACTGATGAGAGCCAGGAGCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCC 198244 TGAGGAGGTAATTATGGCAGTGAGATGAGGATCTGCTTTTGTTAGGGGGTGGGCTGAGG 198484 TAGTACCTCTGCCCCAGGGCACAGTGGGAAGAGGGGCAGAGGGATCTGGCATCCATGGG TCTTCAGTGACCACTCTACGGTGTCGGGCCTTGAACTACTACCCCCAGAACATCACCATG AAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCTAAAGACGTATTG CCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAG CAGAGATATACGINCCAGGIGGAGCACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGG GGTATGTGACTGATGAGAGCCAGGAGCTGAGAAATCTATTGGGGGGTTGAGAGAGTGCC TGAGGAGGTAATTATGGCAGTGAGATGAGGATCTGCTTTTGTTAGGGGGTGGGCTGAGG 198364 TAGTCALTGGAGTCATCAGTGGAATTGCTGTTTTTGTCGTCATCTTGTTGATTGTTGAATTT GTGGCAATCAAAGGCTTTAACTTGCTTTTTTTTTAGAGCCCTCACCGTCTGGCACCC TAGTCATTGGAGTCATCAGTGGAATTGCTGTTTTTGTCGTCATCTTGTTCATTGGAATTT TTTGCAAGAGCTGTTTAAGGTAGTACAGGGGCTTTGAGGGTTGAGAAGTCACTGTGGCTAT AAGCATTTTTCTCATTTATATTCTTTGGGGACACCCAGCAGCTCCCTGGGAGACAGAAAT ACCCCATGAGGTCCTAAAGCAGGAAGCAAATGCTTAGGGTGTCAAAGGAAAGAATG **ATCACATTCAGCTGGGGATCAAGATAGCCTTCTGGATCTTGAAGGAGAAGCTGGATTCCA** TAGTACCTCTGCCCCAGGGCACAGTGGGAAGAGGGGCAGAGGGGATCTGGCATCCATGGG TCTCAGAACCCAAATCTGGTAGGGAATGAAATTGATAGCAAGTAAATGTAGTTAAAGAAG 5701 5881 Db 198004 5761 5821 5941 6001 6061 6181 6241 6301 6361 6421 6481 6541 198544 198604 198664 198724 198784 198844 g ă ŏ ŏλ δy g QΥ g ŏ qq δŏ q δ qq g δy g ò Dp qq δλ Ωp g Вb op οy g Ωp δ á ŏ δ δy δ δy

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24 AGCTATCACTCACCAATTATGCATTTCTACCCCCTGAACATCTGTGGTGTAGGGAAAAGA 199083	81 GAATCAGAAAGACCGCTCATACAGAGTCCAAGGTCTTTTGGGATATTGGGTTATGA 6840 	6841 TCACTGGGGTGTCATTGAAGGATCCTAAGAAAGGAGGACCACGATCTCCCTTATATGGTG 6900 	6901 AATGTGTTGTTAAGAAGTTAGATGAGAGGTGAGGAGACCAGTTAGAAAGCCAATAAGCAT 6960 	6961 TTCCAGATGAGATAATGGTTCTTGAAATCCAATAGTGCCCAGGTCTAAATTGAGATGG 7020 . 	7021 GTGAATGAGGAAAATAAGGAAGAGAGAGAGAGAGAGAGGTGCCTAGGTTTGTGATGCCT 7080 	7081 CTTICCTGGGTCTCTTGTCTCCACAGGAGGACCATGGGCACTACGTCTTAGCTGACG 7140 	7141 TGAGTGACAGCGGCAGCCTGCAGAGCAAGAGAAGAAAAAAAA	7201 GGGAGTGCATTTATGAGCTCTTCATGTTTCAGGAGAGAGTTGAACCTAAACATAGAATT 7260 	7261 GCCTGACGAACTCCTTGATTTTAGCCTTCTCTGTTCATTTCCTCAAAAAGATTTCCCCAT 7320 	321 TTAGGTTTCTGAGTTCCTGCATGCCGGTGATCCCTAGGCTGTGACCTCTCCCCTGGAACTG 7380 	7381 TCTCTCATGAACCTCAAGCTGCTAGAGGCTTCCTTCATTTCCTCCGTCACCTCAGAG 7440 	7441 ACATACACCTATGTTTCCTATTTTGGAAGAGACTCCTTAAATTTGGGGGA 7500 	7501 CTTACATGATTCATTTTAACATCTGAGAAAGCTTTGAACCCTGGGACGTGGCTAGTCAT 7560 	7561 AACCTTACCAGATTTTTACACATGTATCTATGCATTTTTCTGGACCCGTTCAACTTTTCCT 7620 	7621 TTGAATCCTCTCTGTGTTACCCAGTAACTCATCTGTCACCAAGCCTTGGGGATTCTTC 7680 	7681 CATCTGATTGTGATGTGAGTTGCACAGCTATGAAGGCTGTACACTGCACGAATGGAAGA 7740 	7741 GCACCTGTCCCAGAAAAGCATCATGGCTATCTGTGGGTAGTATGATGGTGGTGTTTTTAGC 7800 	7801 AGGTAGGAGCAAATATCTTGAAAGGGGTTGTGAAGAGGTGTTTTTCTAATTGGCATGA 7860
b 19902,	y 6781 b 199084	19	19	19	19	Oy 70 Db 1993	Qy 71 Db 1994	Qy 72 Db 1995	Qy 72 Db 1995	Oy 7321 Db 199624	Oy 73 Db 1996	Oy 74 Db 1997	Oy 75 Db 1998	Qy 75	Oy 76 Db 1999	Qy 76 Db 1999	Oy 7741 Db 200044	0y 7.
QQ	Oy Dp	ç g	Q7 Db	O. Db	9. Pb	O D	0 0	OΩ	0 0	0 0	O D	O D	ОΩ	0 0	0 0	<u>u</u>	5 1	9

AAGTGGAGTAAGCTCTCTCATTTGAGATGGTATAATGGAAGCCACCAAGTG 8940 recentricitaticitaticitaticitaticitaticitaticates 200943 200823 201123 201183 200583 200643 201063 200403 200463 8340 8400 8460 8640 8700 8820 8880 8100 8160 8280 8040 AGGTCCTGGAATGTGACTCCCTTGCTCTTGTTGCTCTTTGGCATTCA JACCCTACGCAAGGACTGTAATTGGTGGGGACAGCTAGTGGCCCTGCTGGGC CAGTGAGCCGAGTTTGCGCCACTGCACTCCAGCCTAGGTGACAGAGTGAGA :TCATAGTTTGTCAGTGATAGAAACAGGTTTCAAACTCAGTCAATCTGACCG ATGGCTCTTCTTCTCTCTCTCTCTCTCTCTCAGTGAGCTTGAATCACAT ACAGCAGAAAACAACCAACTGATCCTCAGCTGTCATGTTTCCTTTAAAAGTC GGTGTCCTCCCTAGGCCAGTGCCTCTGGAGTCAGAACTCTGGTGGTATTTC AGGATGATAAAAGCACTTACTTCGTGTCCGACTCTTCTGAGCACCTACTTA CTGCATGCACTTCTTACAATAATTCTATGAGATAGGTACTATTATCCCCAT AAATGAAGAAAGTGAAGTAGGCCGGGCACGGTGGCTCACGCCTGTAATCCC GTCCCAGCTACTCGGAAGGCTGAGGCAGGAGAATGGCATGAACCCAGGAGG SAAGAATCACAATAATTTTCTACCTGGTCTCTCCTTGTTCTGATAATGAAA

8941 01244	GCTTAGAGGATGCCCAGGTCCTTCCATGGAGCCACTGGGGTTCCGGTGCACATTAAAAAA 9000
9001	AAAATCTAACCAGGACATTCAGGAATTGCTAGATTCTGGGAAATCAGTTCACCATGTTCA 9060
9061 201364	AAAGAGTCTTTTTTTTTTTTGAGACTCTATTGCCCAGGCTGGAGTGCATGAT 9120
9121	CTCGGCTCACTGTAACCTCTCCCAGGTTCAAGCGATTCTCCTGTCTCAGCCTCCCA 9180
9181 201484	AGTAGCTGGGATTACAGGCGTGCACCATGCCCGGCTAATTTTTGTATTTTTAGTAG9 9240
9241 201544	GACAGGGTTTCACCARGTTGCCCAGGTGGTCTCGAACTCTCCTGACCTCGTGATCCGCC 9300
9301 201604	TGCCTCGGCCTCCCAAAGTGCTGACATTACAGGTGTGAGCCACCCTGCCCAGCCGTCAA 9360
9361 201664	AGAGTCTTAATATATATATCCAGATGCCATGTGTTTACTTATGTTACTACACTGCACTTG 9420
9421	GCTGCATAAATGTGGTACAAGCATTCTGTCTTGAAGGGCAGGTGCTTCAGGATACCATAT 9480
9481 201784	ACAGCICAGAAGTITCITCITTAGGATTAAAITTIAGGAAAGATAICTCAICITCIT 9540
9541 201844	TTAAACCATTTTCTTTTTTTGGGTTAGAAAGTTATGTAGAAAAAAGTAAATGTGATTT 9600
9601 201904	ACGCTCATTGTAGAAAAGCTATAAAATGAATACAATTAAAGCTGTTATTTAATTAGCCAG 9660
9661 201964	TGAAAAACTATTAACAACTTGTCTATTACCTGTTAGTATTATTGTTGCATTAAAAATGCA 9720
9721	TATACTITAATAAATGTATATIGTATIGTATACTGCATGATTITATIGAAGTICTIGTIC 9780
9781	ATCTTGTGTATATACTTAATCGCTTTGTCATTTTGGAGACATTTATTT
9841 202144	CTTTACATTTTGTCTTACGGAATATTTCATTCAACTGTGGTAGCCGAATTAATCGTGTT 9900
9901	TCTTCACTCTAGGGACATTGTCGTCTAAGTTGTAAGACATTGGTTATTTTACCAGCAAAC 9960
9961 202264	CATTCTGAAAGCATATGACAAATTATTTCTCTTAATATCTTACTATACTGAAAGCAGA 10020

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202324 CIGCIATAAGGCTICACTIACTCTTCTACCTCATAAGGAATAIGTTACAATTAATTTATT
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                                                                         GTTAATTTTTTAATAGAAATTTTAAGTCCTCATTTTCGGTGTTTTTTAAGCTTAA
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                                                          AGGTAAGCATTTGTTTTATATTGGTTTTTATTTCACCTGGGCTGAGATTTCAAGAAACACC
                                                                                                                   10141 CCAGICTICACAGIAACACATITCACIAACACATITACIAAACAICAGCAACIGIGGCCI
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Patent No. 587237

GENERAL INFORMATION:
APPLICANT: Edet. John N.
APPLICANT: Ender, Peter M.
APPLICANT: Tundy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Thomas, Winston
APPLICANT: Thomas, Winston
APPLICANT: Thomas, Waston
APPLICANT: Thomas, Waston
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Sequences and Antibodies Thereto
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
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Pred. No. 0;
0; Mismatches
                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
RPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                           ; NAME/KEY: misc_feature
; LOCATION: 1..246240
; OTHER INFORMATION: /note= "HLA-H.CONTIG"
US-08-724-394A-22
TOWNSEND and
             Center, 8th
                                                                                                                                                                              CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: FILE, Renee, 35,136
REFERENCE/DOCKET NUMBER: 0179;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0300
                                                                                                                                                                                                                                                                                                                  LENGTH: 246240 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
100.0%;
                                                                                                                                                                                                                                                                            TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
 and
           : Two Embarcadero
San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 10823; Conservative
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                                                               94111-3834
                                                    usa
                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                          CITY: Sal
STATE: CA
COUNTRY:
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DD 193204 GGTTTCCACACACGAAGGAATGCGTTGGGCGGGGGGGCGCGAAAGAGTGGCGTTGGGGA 193263
CAAATTATTCAATGGTACACTGGCCTTTGGTGCAGAGCTCATGTCTCCACTTCATAGC 1620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TAATGAACATGTAAGGAATGCACTCACTTCTAAGTTACATTCATATCTGATCTTATTTGA 1260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTTTCACTAGGCATAGGGAGGTAGGAGCTAATAATACGTTTATTTTACTAGAAGTTAACT
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                                                                                                                                                                                                                                            TAAATAAATCTCGTAGTTCCTCACTTGAGCTGAGCTAAGCCTGGGGCTCCTTGAACCTGG
                                                                                                                                                                                                                                                               DD 193024 TAMATAMATCTCGTAGTTCCTCACTTGAGCTGAGCTAAGCCTGGGGCTCCTTGAACCTGG
                                                                                                                                                                                                                                                                                                                              DD 193084 AACTCGGGTTTATTCCAATGTCAGCTGTGCAGTTTTTTCCCAGTCATCTCCAAACAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1021 GGGAGGCTCCTGAGAGGCCTACCTCGGGCCTTTCCCCCACTCTTGGCAATTGTTCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            193324 GGGAGGCTCCTGAGAGGCCTACCCGGGCCTTTCCCCACTCTTGCCAATGTTCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTAGGCTTTATTGAATTGCAATGTGCTGTGTAATTAAGAGGCCTCTCTACAAAGTACTGA
                                                                                                                                                                                                                                                                                                           AACTCGGGTTTATTTCCAATGTCAGCTGTGCAGTTTTTTCCCCAGTCATCTCCAAACAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCTGAATTCTTCACCATTCCACCCACTTTTGGTGAGACCTGGGGTGGAGGTCTTAGGGT
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                                                                                                                                                                            192844 TCAACCCTATCCGCAAGCCCCTCTCCCTACTTTCTGCGTCCAGACCCCGTAAGGGAGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                             901 GGTTTCCACCTCAGAACGAATGCGTTGGGCGGTGGGGGCGCGCGAAAGAGTGGCGTTGGGGA
                                                                                                                 CTACCACTGAACTGCAGATAGGGGTCCCTCGCCCCAGGACCTGCCCCCCTCCCCCGGCTGT
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93923	680 93983	740 94043	00	860 94163	920 94223	980 94283	040 94343	100 94403	160 94463	220 94523	280 94583	340 94643	400 94703	460 94763	;20 ;4823	180 14883	4943	.00 15003
CAAATTTATTCAATGGTACACTGGGCTTTGGTGGCAGAGCTCATGTCTCCACTTCATAGC 1	TATGATTCTTAAACATCACACTGCATTAGAGGTTGAATAATAAAATTTCATGTTGAGCAG 1. 	AAATATTCATTGTTTACAAGTGTAAATGAGTCCCAGCCATGTGTGCGCTGTTCAAGCC 1	AAGTCTTTACCCTTTGATATTTTGCATTCTAGTGGGAGA 1.	GATGACAATAAGCAAATGAGCAGAAAGATATACAACATCAGGAAATCATGGGTGTTGTGA 	GAAGCAGAGAAGTCAGGGCAAGTCACTGGGGGCTGACACTTGAGCAGAGACATGAAGA 19 	AATAAGAATGATATTGACTGGGAGCAGTATTTCCCAGGCAAACTGAGTGGGCCTGGCAAG 19 	TTGGATTAAAAAGGGGGTTTTCTCAGCACTACTCATGTGTGTG	CGGCGTGGGGGGAAGGGGAACTACCATCTGCATGTAGGATGTCTAGCAGTATCCTGT 21 	CCTCCCTACTCACTAGGTGCTAGGAGCACTCCCCCGGTCTTGACAACCAAAAATGTCTCT 21 	AAACTTTGCCACATGTCACCTAGTAGACAAACTCCTGGTTAAGAAGCTCGGGTTGAAAA 22 	AATAAACAAGTACTGCGGGGGTAGAGGCCCAAGAAGTAGGTAATGGGCTCAGAAGAGG 23 	GCCACAAACAAGGIIGIGCAGGCGCCTGIAGGCIGTGGIGTGAATICTAGCCAAGGAGIA 23 	ACAGTGATCTGTCACAGGCTTTTAAAAGATTGCTCTGGCTGCTATGTGGAAAGCAGAATG 24 	AAGGGAGCAACAGTAAAAGCAGGGAGCCCAGCAGGAAGCTGTTACACAGTCCAGGCAAG 24 	AGGTAGTGGAGTGGGTGGGGAACAGAAAAGGGAGTGACAAACCATTGTCTCCTGAA 25 	TATATICTGAAGGAAGTIGCIGAAGGATICTAIGTIGIGGAGAGAAAAGAGAATIGG 25 	CTGGGTGTAGTAGCTCATGCCAAGGAGGCCAAGGAGAGAGA	GTTCAAGACCAGCCTGGGCAACACAGCAAAACCCCTTCTCTACAAAAATACAAAATTA 27
Db 193864	Oy 1621 Db 193924	Qy 1681 Db 193984	Oy 1741 Db 194044	Qy 1801 Db 194104	Qy 1861 Db 194164	Oy 1921 Db 194224	Qy 1981 Db 194284	Qy 2041 Db 194344	Oy 2101 Db 194404	Oy 2161 Db 194464	Oy 2221 Db 194524	Oy 2281 (DD 194584 (Oy 2341 Db 194644	Qy 2401 i	Oy 2461 i Db 194764 i	Oy 2521 g	QY 2581 (DD 194884 (Qy 2641 (

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Š	7/0	GCTGGGTGTGGTGGTGCACCTGTGATCCTAGCTACTCGGGAGGCTGAGGTGGAGGGTA	2760
අධ	195	CTGGGTGTGGCATGCACCTGTGATCCTAGCTACTCGGGAGGCTGAGGTGGAGGGT	195063
οy	27	TIGCTTGAGCCCAGGAAGTTGAGGCTGCAGTGAGCCATGACTGTGCCACTGTACTTCAGC	2820
ď	b 195064	GCTTGAGCCCAGGAAGTTGAGGCTGCAGTGAGCCATGACTGTGCCACTGTGTTCAG	195123
Qy	2821	CAAGACCCTGTCTCCCCTGACAAAAAAAAGAAGTTT	2880
qq	195124		195183
Qy	2881	GACTITGITCTITATITITAATITTAATIGGCCTGAGCAGTGGGGTAATIGGCAATGC	2940
qq	195184	TTGTTCTTATTTAATT	195243
Qy	, 2941	CAGAGGAAAGGACAGTTTGGGGTAAATCAAGGATCTGCATTT	3000
qq	195244	CTGAGATGGTGAAGGCAGA	195303
ΟY	3001	GTGAGGCCACATAGG	3060
qa	195304	GACATGTTAAGTTTGAGATTCCAGTCAGGCTTCCAAGTGGTGAGGCCACATAGGCA	195363
δλ	3061	AGTGTAAGAATTCAGGACCAAGGCTGGGCACGGTGGCTCACTTCTGTAATCCCAGCA	3120
qq	195364	TGTAAGAATTCAGGACCAAGGCTGG	195423
δλ	3121	SAGACAAGCTTGGC	3180
qq	195424	TGGTGGCTGAGGCAGGTAGATCATTTGAGGTCAGGAGTTT	195483
Qy	3181	TGGTGAAACCCCATGTCTACTAAAAATACAAAAATTAGCCTGGTGTGGTGGCGCACGCCT	3240
QΩ	195484	GGTGAAACCCCATGTCTACTAAAATACAAAAATTAGCCTGGTGTGGTGGTGGCGCACG	195543
δλ	3241	CAGGAGGT	3300
đ	195544	ICCCAGGTTTTCAGGAGGCTTAGGTAGGAGAATCCCTTGAACCCAGGAGGTGCAG	195603
δy	3301	TIGCAGTGAGCTGAGATTGTGCCACTGCACTCCAGCCTGGGTGATAGAGTGAGACTCTGT	3360
qq	195604	SCAGTGAGCTGAGATTGTGCCACTGCACTCCAGCCTGGGTGATAGAGTGAGACTCT	195663
δy	3361	CTCAAAAAAAAAAAAAAAAAAAAAAAAAACTGAAGGAATTATTCCTCAGGATTTGGG	3420
qa	195664	CARARARARARARARARARARARARARARARARARARAR	195723
QY	3421	CTGAGTTCAACTACCATGGCTAGACACCCTTAA	3480
qq	195724	AATTTGCCCTGAGCACCAACTCCTGAGT	195783
Qy	3481	SGAGTCTGTCTAATCATGAGTATTGGAATAG	3540
q	195784	TTCTAGAATCCACCAG	195843
ΟY	3541	GGGGCAGTGAGGGGGGGCAGCCACGTGTGGCACAGAAAAGCACACAAAGGAAAGAG	3600
qq	195844	GGGGCAGT	195903
QY	3601	SACTGTCATATGGAAAAAAAGACAGGACTGCAACTCACCCTTCACAAAATG	3660
qa	195904	CAGGACTGT	195963
Οŷ	3661	CCAGACACACAGGTGATGAGTTGATGCAGGTGTGTGGGGGCCTCAACATCCTGCTCCC	3720
đ	195964	AGACACAGGTGATGGTTGATGTTGATGTGTGTGTGGAGCCTCAACATCCTGCTCCC	196023
QY	3721	CTCCTACTACACATGGTTAAGGCCTGTTGCTCTGTCTCCAGGTTCACACTCTCTGCACTA	3780
qq	196024	CCTACTACACATGGTTAAGGCCTGTTGTTGTTTTTTTTTT	196083

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3840 19614:	3900 19620	3960 19626:	4020 19632:	4080	4140	4200 19650	4260 19656	4320 19662	4380 19668	4440 19674	4500 19680	4560 19686	4620 19692	4680 19698	4740 19704	4800 19710	4860	4920
CCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCTTGTTTGAAGCTTTGGGCTA 	CGTGGATGACCAGCTGTTCGTGTTCTATGATNATGAGAGTCGCCGTGTGGAGCCCCGAAC 	TCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGCAGCTGAGTCAGAGTCTGAA 	AGGGGGGATCACATGTTCACTGTTGACTTCTGGACTATTATGGAAAATCACAACCACAG 	CAAGGGIAIGTGGAGAGGGGCCTCACCTTCCTGAGGTTGTCAGAGCTTTTCATCTTTC 	atgcatcttgaaggaaacagctggaagtctgaggtcttgtgggaagcagggaagagggaag 	GAATTTGCTTCCTGAGATCATTTGGTCCTTGGGGATGGTGGAAATAGGGACCTATTCCTT 	TGGTTGCAGTTAACAAGGCTGGGGATTTTTCCAGAGTCCCACACCCTGCAGGTCATCTG 	GGCTGTGAAATGCAAGAAGACAGTACCGAGGGCTACTGGAAGTACGGGTATGATGGG 	CAGGACCACCTTGAATTCTGCCCTGACACACTGGATTGGAGAGCAGCAGAACCCAGGGCC 	TGGCCCACCAAGCTGGAGTGGGAAAGGCACAAGATTCGGGCCAGGAGAACAGGGCCTAC 	CTGGAGAGGACTGCCCTGCACAGCTGCAGCAGTTGCTGGAGCTGGGGAGAGGTGTTTTG 	GACCAACAAGGTAIGGIGGAAACACACIICIGCCCCTATACICTAGIGGCAGAGIGGAGGGGGGGGGG	AGGTTGCAGGGCACGGAATCCCTGGTTGGAGTTTCAGAGGTGGCTGAGGCTGTGTGCCTC	TCCAAATTCTGGGAAGGGACTTTCTCAATCCTAGAGTCTCTACCTTATAATTGAGATGTA 	TGAGACAGCCACAAGTCATGGGTTTAATTTCTTTTCTCCATGCATATGGCTCAAAGGAA 	GFGFCTATGGCCCTTGCTTTTTATTTAACCAATAATCTTTTGTATATTTATACCTGTTAA GTGTCTATGGCCCTTGCTTTTTATTTAACCAATAATCTTTTGTATTTATACCTGTTAA	AAATTCAGAAATGTCAAGGCCGGGCACGGTGGCTCACCCCTGTAATCCCAGCACTTTGGGTIIIIIIIIII	CAGGCGGGTGGTCACAAGGTCAGGAGTTT
3781 196084	3841	3901	3961 196264	4021	4081	4141	4201	4261	4321	4381	4441	4501	4561	4621 196924	4681 196984	4741	4801	486
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197884 CTCATCCTTTCCTGTCAAGTGCCTCCTTTGGTGAAGGTGACACATCATGTGACC 197943 198064 CCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAG 198123 197883 198183 GCTAATTGGAAGGCTGAGGCAGGACCATCGCTTGAACCTGGGAAGCGGAAGTTGCACTGA 5040 --Db 197404 AAAAAAAAAAAAAAAAAAAAAAAATTCAGAATCTCAGCTATCATATGAATACCAGGACAAA 197463 197763 5400 5640 5760 5941 IGAGGAAGTAATTATGGCAGTGAGATCTGCTCTTTTTTTTAGGGGGTGGGCTGAGG 6000 5100 197824 AACCTAIAGAAGGAAGIGAAAGTICCAGICTICCIGGCAAGGGTAAACAGAICCCCICTC AAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCTAAAGACGTATTG CCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAG Db 197344 GCCAAGACCACTGCACTCCAGCCTAGGCAGAGAGAGAGACTCCATCTTAAAAAA AGGGCAATTTTATCTATCAGAACAAGAACATGGGTAACAGATATGTATATTTACATGTG 197644 AGGGCAATTTTATCTATCAGAACAAGAACATGGGTAACAGATATGTATTTACATGTG AGGAGAACAAGCTGATCTGACTGCTCTCCAAGTGACACTGTGTTAGAGTCCAATCTTAGG 197704 AGGAGAACAAGCTGATCTGACTGCTCTCCAAGTGACACTGTGTTAGAGTCCAATCTTAGG AACCTATAGAAGGAAGTGAAAGTTCCAGTCTTCCTGGCAAGGGTAAACAGATCCCCTCTC CTCATCCTTCCTCTTTCCTGTCAAGTGCCTCCTTTGGTGAAGGTGACACATCATGTGACC TCTTCAGTGACCACTCTACGGTGTCGGGCCTTGAACTACTCCCCCAGAACATCACCATG GCCAAGATCGCGCCACTGCACTCCAGCCTAGGCAGCAGGAGTGAGACTCCATCTTAAAAAA **AAAAAAAAAAAAAAAAAAAGAGATTCAGAGATCTCAGCTATCATATGAATACCAGGACAAA** AGAACATAGCAATAATCACTGAAGCTACCTATCTTACAAGTCCGCTTCTTATAACAATGC **ACCCGTCTCTAAAAAAATACAAAATTAGCTGGTCACAGTCATGCGCACCTGTAGTCCCA** 5461 5581 5701 5761 5341 5401 5521 5641 4981 5041 5101 5161 5221 Db 197524 Db 197164 Db 197284 4921 197224 g q Dp qq g qq g g Dp ōλ οy ŏ δ ò ŏ δý ŏ ò Qγ q δ à Qγ οy Qγ δ Qγ ò

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198303	6060 198363	6120 198423	6180 198483	6240 198543	6300 198603	6360 198663	6420 198723	6480 198783	6540 198843	6600 198903	6660 198963	6720 199023	6780 199083	6840 199143	6900 199203	6960 199263	7020 199323	7080 199383
TGAGGAGGTAATTATGGCAGTGAGATGAGGATCTGCTCTTTGTTAGGGGGTGGGCTGAGG	GTGGCAATCAAAGGCTTTAACTTGCTTTTTCTGTTTTAGAGCCCTCACCGTCTGGCACCC	TAGTCATTGGAGTCATCAGTGGAATTGCTGTTTTTGTCGTCATCTTGTTCATTGGAATTT	TGTTCATAATATTAAGGAAGAGGCAGGGTTCAAGTGAGTAGGAACAAGGGGGAAGTCTCT 	TAGTACCTCTGCCCCAGGGCACAGTGGGAAGAGGGGCAGAGGGGGTTCTGGCATCCATGGG 	AAGCATTTTCTCATTTATATTCTTTGGGGACACCAGCAGCTCCCTGGGAGACAGAAAT 	AATGGTTCTCCCCAGAATGAAAGTCTCTAATTCAACAACATCTTCAGAGCACCTACTAT	TTTGCAAGAGCTGTTTAAGGTAGTACAGGGGCTTTGAGGTTGAGAAAGTCACTGTGGCTAT 	TCTCAGAACCCAAATCTGGTAGGGAATGAAATTGATAGCAAGTAAATGTAGTTAAAGAAG 	ACCCATGAGGTCCTAAAGCAGGCAGGAAATGCTTAGGGTGTCAAAGGAAGAATG	ATCACATTCAGGTGGGGATCAAGATAGCCTTCTGGATCTTGAAGGAGAAGAGGTGGATTCCA 	TTAGGTGAGGTTGAAGATGATGGAGGTCTACACAGAGGGGGGCACCATGCCAAGTAGGA 	GAGTATAAGGCATACTGGGAGATTAGAAATAATTACTGTACCTTAACCCTGAGTTTGCGT 	AGCTATCACTCACCAATTATGCATTTCTACCCCCTGAACATCTGTGGTGTAGGGAAAAGA 	GAATCAGAAAGAAGCCAGCTCATACAGAGTCCAAGGGTCTTTTGGGATATTGGGTTATGA 	TCACTGGGGTGTCATTGAAGGATCCTAAGAAAGGAGGACCACGATCTCCCTTATATGGTG	AATGTGTTGTTAAGAAGTTAGATGAGAGGTGAGGAGACCAGTTAGAAAGCCAATAAGCATA 	TTCCAGATGAGAGATAATGGTTCTTGAAATCCAATAGTGCCCAGGTCTAAATTGAGATGG 	GTGAATGAGGAAAATAAGGAAGAGAGAGAGGCAAGATGGTGCCTAGGTTTGTGATGCCT
198244	6001 198304	, 6061) 198364	, 6121) 198424	6181	6241 198544	6301	6361	6421	6481	6541	6601	6661 198964	6721 199024	6781 199084	6841 199144	6901 199204	6961 199264	7021 199324
op.	Q P	QY Db	Qy Db	QY	QY Db	Oy Db	QQ QQ	9y Db	Qy Dp	Oy Dp	Qy Dp	Oy Dp	Qy Db	S S	QY Db	QY Db	δγ Dp	Q D

31 CTTTY 34 CTTTY 35 CTTTY 35 CTTTY 36 CTTTY 36 CTTTY 37 CTTTY 37 CTTY 37 CTTY 38 CTTTY 38 CTTTY 39 CTTTY 31 CTCTY 31 CTTAG 31 CT	281
	199334 7 714 7 726 19956 19965 19965 19966 19966 19966 19966 19966 19974 762 19998 19998 762 19998 762 762 768 768 768 778 778 778 778 778

201544 9301 201604 9361 201664 9421 9421 201724 9481 201784 9601 201904 9601 202024 9721 202024 9901 202264 10021 10081 202324	OY 10251 THITCH DD 202564 THITTCH QY 10321 CATTITE
ACCACTITICGGRIGGCCAAAGCGGGGGATTCACGGGGTCGGGAAATCGGGGCCACTCCGGG 20152 ACCACTITICGGRIGGCCAAAGCGGGTGAATCACGGGGTCAGGGAATCGGGACCACTCGG 20152 TACATGGTGAAACCCCAATCATAAAATCACAAAATTACTGGGCACTGGGCACGGGGG 20153 TACATGGTGAAACCCCACTCTCTAAAAATCACAAAATTACTGGGCACTGGGCGCG 20153 ACCCCTGTGATCCCAGCTACTCCAGAAAATCACAAAATTACTGGGCATGAACCAGGGG 20163 ACCCCTGTGATCCCAGCTACTCCAGAAAATCACAGGAATGGCATGAACCAGGGG 20163 ACCCCTGTAACCCCAGTACTCCAGAGGCTGAACAGGAATGGCATGAACCCAGGGG 20163 ACCCCTGTAACCAGGAACCCCAGTCAACACGAGGAATGGCATGAACCAGGAGG 8140 ACCCCTGTAACCAGGAACCCCAGTCAACACGAGGAATGGCATGAACCCAGGGG 20163 ACCCCTGTAACACAGGAACCCAGTCAACACGAGGAATGGCATGAACCCAGGGG 20163 ACCCCTGTAACAAAAATAAAAATAAAAAAAAAAAAAAAA	11 AGTAGCTGGGATTACAGGCGTGCACCACCATGCCCGGCTAATTTTTGTATTTTTAGTAGG 9240
QY 8161 DD 200464 QY 8221 DD 200524 QY 8281 DD 200584 QY 8401 DD 200764 QY 8461 DD 200764 QY 8521 DD 200824 QY 8701 DD 201004 QY 8761 DD 201124 QY 8821 QY 8881 QY 8881 QY 8941 DD 201184 QY 8941 DD 201304 QY 9061 QY 9121 QY 9121	Oy 9181 Db 201484 Oy 9241

ABATTCTTATTCACCTCTGGCAAACCATTCACAAACCATGGTAGTAAAGAGA 10380 GCATTTGTTTTATATTGGTTTTATTTTCACCTGGGCTGAGATTTCAAGAAACAC TTCACAGTAACACATTTCACTAACACATTTACTAAACATCAGCAACTGTGGCCT TITITIAATAGAAATITITAAGTCCTCATITITCTITCGGTGTTTTTTAAGCTTAA SGCCTCCCAAAGTGCTGAGATTACAGGTGTGAGCCACCCTGCCCAGCCGTCAAA **ATTGTAGAAAAGCTATAAAATGAATACAATTAAAGCTGTTATTTAATTAGCCAG** ACTATTAACAACTTGTCTATTACCTGTTAGTATTATTGTTGCATTAAAAATGCA TTAATAAATGTATATTGTATTGTATACTGCATGATTTTATTGAAGTTCTTGTTC ATTTTGTCTTACGGAATATTTTCATTCAACTGTGGTAGCCGAATTAATCGTGTT TTAATATATATATCCAGATGGCATGTGTTTTACTTTATGTTACTACATGCACTTG

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ם ט	.; ₽	10381 202684	GGGTGACACCTGGTGGCCATAGGTAAATGTACCACGGTGGTCCGGTGACCAGAGATGCAG 	10440 202743
O D	ζζ Ωρ	10441	CGCTGAGGGTTTTCCTGAAGGTAAAGGAATAAAGAATGGGTGGAGGGGCGTGCACTGGAA 	10500 202803
םיט	.; qa	Qy 10501 Db 202804	ATCACTTGTAGAGAAAAGCCCCTGAAAATTTGAGAAAACAAAC	10560 202863
O D	λ. q.	Qy 10561 Db 202864	CTATITGAATIGCTGGAATCACAGGCCATIGCTGAGCTGCCTGAACTGGGAACACAAGAGTGCTGTGAACTGGGAACACAAGAGCTGCTGAACTGGGAACACAAGAGCCATTGCTGAACTGGGAACAACAACAG	10620 202923
<i>3</i>	% ₽	Oy 10621 Db 202924	AAGGAAAACAACCACTCTGATAATCATTGAGTCAAGTACAGCAGGTGATTGAGGACTGC 	10680 202983
O D	ζς QΩ	10681 202984	TGAGAGGTACAGGCCAAAATTCTTATGTTGTATTATAATAATGTCATGTTATAATAGTGT 	10740 203043
0 0	. q	Oy 10741 Db 203044	CAGTATTTTATAAAACATTCTTCACAAACTCACACATTTAAAAACAAAACAGGGTGTCTC 	10800 203103
J D	ζζ Oγ	10801	TAAAATCCCAAATTTTCATAAAC 10825 	

Search completed: June 19, 2002, 18:01:11 Job time: 14623 sec